

## SEQUENCE LISTING

&lt;110&gt; Garvan Institute of Medical Research

&lt;120&gt; Methods for the diagnosis and prognosis of ovarian cancer

&lt;130&gt; 501731/MRO

&lt;150&gt; AU2002951346

&lt;151&gt; 2002-09-05

&lt;160&gt; 84

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 3432

&lt;212&gt; DNA

&lt;213&gt; NM\_005460 SNCAIP, synphilin

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&lt;221&gt; CDS

&lt;222&gt; (94)..(2850)

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Gly Ile Ala Asp Val Tyr Ser Lys Phe Arg Pro Val Lys Arg Val Ser
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Pro Leu Lys His Gln Pro Glu Thr Leu Glu Asn Asn Glu Ser Asp Asp
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Gln Lys Asn Gln Lys Val Val Glu Tyr Gln Lys Gly Gly Glu Ser Asp
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Ile Leu Gly Leu Cys Thr Thr Ile Asn Gly Leu Ser Gly Lys Ala Cys
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Met Asn Ser Gly Val  
1 5  
gcc atg aaa tat gga aac gac tcc tcg gcc gag ctg agt gag ctc cat 283  
Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu Leu Ser Glu Leu His  
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Ala Lys Ala Gln Cys Glu Ser His Leu Met Arg Glu His Glu Asp  
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Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu Arg Ile Thr Glu Leu  
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gag cag agg ctg aag gat tat atc cag cag ctc aag aat gac agg gct Glu Gln Arg Leu Lys Asp Tyr Ile Gln Gln Leu Lys Asn Asp Arg Ala 570 575 580	1963
gcg gtc aag ctg acc atg ctg gag ctg gaa agc atc cac atc gat cct Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser Ile His Ile Asp Pro 585 590 595	2011
ctc agc tat gac gtc aag cct cgg gga gac agc cag agg ctg gat ctg Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser Gln Arg Leu Asp Leu 600 605 610	2059
gaa aac gca gtg ctt atg cag gag ctc atg gcc atg aag gag gag atg Glu Asn Ala Val Leu Met Gln Glu Leu Met Ala Met Lys Glu Glu Met 615 620 625	2107
gcc gag ttg aag gcc cag ctc tac cta ctg gag aaa gag aag aag gcc Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu Lys Glu Lys Lys Ala 630 635 640 645	2155
ctg gag ctg aag ctg agc acg cgg gag gcc cag gag cag gcc tac ctg Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln Glu Gln Ala Tyr Leu 650 655 660	2203
gtg cac att gag cac ctg aag tcc gag gtg gag gag cag aag gag cag Val His Ile Glu His Leu Lys Ser Glu Val Glu Glu Gln Lys Glu Gln 665 670 675	2251
cgg atg cga tcc ctc agc tcc acc agc agc ggc agc aaa gat aaa cct Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly Ser Lys Asp Lys Pro 680 685 690	2299
ggc aag gag tgt gct gat gct gcc tcc cca gct ctg tcc cta gct gaa Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala Leu Ser Leu Ala Glu 695 700 705	2347
ctc agg aca acg tgc agc gag aat gag ctg gct gcg gag ttc acc aac Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala Ala Glu Phe Thr Asn 710 715 720 725	2395
gcc att cgt cga gaa aag aag ttg aag gcc aga gtt caa gag ctg gtg Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg Val Gln Glu Leu Val 730 735 740	2443
agt gcc ttg gag aga ctc acc aag agc agt gaa atc cga cat cag caa Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu Ile Arg His Gln Gln 745 750 755	2491
tct gca gag ttc gtg aat gat cta aag cgg gcc aac agc aac ctg gtg Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala Asn Ser Asn Leu Val 760 765 770	2539

gct gcc tat gag aaa gca aag aaa aag cat caa aac aaa ctg aag aag	2587
Ala Ala Tyr Glu Lys Ala Lys Lys Lys His Gln Asn Lys Leu Lys Lys	
775 780 785	
tta gag tcg cag atg atg gcc atg gtg gag aga cat gag acc caa gtg	2635
Leu Glu Ser Gln Met Met Ala Met Val Glu Arg His Glu Thr Gln Val	
790 795 800 805	
agg atg ctc aag caa aga ata gct ctg cta gag gag gag aac tcc agg	2683
Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu Glu Glu Asn Ser Arg	
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cca cac acc aat gaa act tcg ctt taatcagcac tcacgcaccg gagttctgcc	2737
Pro His Thr Asn Glu Thr Ser Leu	
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catgggaagt aaactgcagc aggccactgg ggacagaagg gcccatgtac ttgttgggag	2797
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cagg	4181



&lt;210&gt; 4

&lt;211&gt; 829

&lt;212&gt; PRT

&lt;213&gt; NM\_002387 MCC, mutated in colorectal cancers

&lt;400&gt; 4

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Leu Ser Glu Leu His Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile  
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Val Glu Leu Asn Lys Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu  
 35 40 45

Leu Glu Lys Lys Leu Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met  
 50 55 60

Arg Glu His Glu Asp Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu  
 65 70 75 80

Arg Ile Thr Glu Leu His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile  
 85 90 95

Asp Arg Leu Gln Gly Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu  
 100 105 110

Leu Arg Ser Glu Leu Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser  
 115 120 125

Arg Ser Met Asp Gln Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln  
 130 135 140

Ser Thr Met Val Thr Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser  
 145 150 155 160

Glu Leu Gln Arg Val Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg  
 165 170 175

Lys Lys Ser Ser Cys Ser Leu Ser Val Ala Glu Val Asp Arg His Ile  
 180 185 190

Glu Gln Leu Thr Thr Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr  
 195 200 205

Val Glu Glu Ile Glu Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu  
 210 215 220

Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu  
225 230 235 240

Glu Asn Glu Ser Leu Thr Ala Met Leu Cys Ser Lys Glu Glu Glu Leu  
245 250 255

Asn Arg Thr Lys Ala Thr Met Asn Ala Ile Arg Glu Glu Arg Asp Arg  
260 265 270

Leu Arg Arg Arg Val Arg Glu Leu Gln Thr Arg Leu Gln Ser Val Gln  
275 280 285

Ala Thr Gly Pro Ser Ser Pro Gly Arg Leu Thr Ser Thr Asn Arg Pro  
290 295 300

Ile Asn Pro Ser Thr Gly Glu Leu Ser Thr Ser Ser Ser Ser Asn Asp  
305 310 315 320

Ile Pro Ile Ala Lys Ile Ala Glu Arg Val Lys Leu Ser Lys Thr Arg  
325 330 335

Ser Glu Ser Ser Ser Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser  
340 345 350

Ser Ile Gly Val Ser Ser Ser Val Ala Glu His Leu Ala His Ser Leu  
355 360 365

Gln Asp Cys Ser Asn Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His  
370 375 380

Gly Ser Ala Ile Ser Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr  
385 390 395 400

Glu Arg Leu Asn Ser Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu  
405 410 415

Leu Thr Ile Thr Leu Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser  
420 425 430

Met Leu Val Gly Lys Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala  
435 440 445

Leu Gln Tyr Ser Glu Gln Cys Ile Glu Ala Tyr Glu Leu Leu Ala  
450 455 460

Leu Ala Glu Ser Glu Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala  
465 470 475 480

Gly Val Gly Ser Ser Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr  
485 490 495

Gln Met Leu Lys Arg Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala  
500 505 510

Ala Lys Ala Leu Leu Met Lys Leu Asp Gly Ser Cys Gly Gly Ala Phe  
515 520 525

Ala Val Ala Gly Cys Ser Val Gln Pro Trp Glu Ser Leu Ser Ser Asn  
530 535 540

Ser His Thr Ser Thr Thr Ser Ser Thr Ala Ser Ser Cys Asp Thr Glu  
545 550 555 560

Phe Thr Lys Glu Asp Glu Gln Arg Leu Lys Asp Tyr Ile Gln Gln Leu  
565 570 575

Lys Asn Asp Arg Ala Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser  
580 585 590

Ile His Ile Asp Pro Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser  
595 600 605

Gln Arg Leu Asp Leu Glu Asn Ala Val Leu Met Gln Glu Leu Met Ala  
610 615 620

Met Lys Glu Glu Met Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu  
625 630 635 640

Lys Glu Lys Lys Ala Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln  
645 650 655

Glu Gln Ala Tyr Leu Val His Ile Glu His Leu Lys Ser Glu Val Glu  
660 665 670

Glu Gln Lys Glu Gln Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly  
675 680 685

Ser Lys Asp Lys Pro Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala  
690 695 700

Leu Ser Leu Ala Glu Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala  
705 710 715 720

Ala Glu Phe Thr Asn Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg  
725 730 735

Val Gln Glu Leu Val Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu  
740 745 750

Ile Arg His Gln Gln Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala  
755 760 765

Asn Ser Asn Leu Val Ala Ala Tyr Glu Lys Ala Lys Lys Lys His Gln  
 770 775 780

Asn Lys Leu Lys Lys Leu Glu Ser Gln Met Met Ala Met Val Glu Arg  
 785 790 795 800

His Glu Thr Gln Val Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu  
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Glu Glu Asn Ser Arg Pro His Thr Asn Glu Thr Ser Leu  
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<212> DNA

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<222> (130)..(2208)

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 gcggtcgcc atg gac cgc cca gat gag ggg cct ccg gcc aag acc cgc cgc 171  
 Met Asp Arg Pro Asp Glu Gly Pro Pro Ala Lys Thr Arg Arg  
 1 5 10  
 ctg agc agc tcc gag tct cca cag cgc gac ccg ccc ccg ccg ccg 219  
 Leu Ser Ser Ser Glu Ser Pro Gln Arg Asp Pro Pro Pro Pro Pro Pro  
 15 20 25 30  
 ccg ccg ccg ctc ctc cga ctg ccg ctg cct cca ccc cag cag cgc ccg 267  
 Pro Pro Pro Leu Leu Arg Leu Pro Leu Pro Pro Pro Gln Gln Arg Pro  
 35 40 45  
 agg ctc cag gag gaa acg gag gcg gca cag gtg ctg gcc gat atg agg 315  
 Arg Leu Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg  
 50 55 60  
 ggg gtg gga ctg ggc ccc gcg ctg ccc ccg ccg cct ccc tat gtc att 363  
 Gly Val Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Pro Tyr Val Ile  
 65 70 75  
 ctc gag gag ggg ggg atc cgc gca tac ttc acg ctc ggt gct gag tgt 411  
 Leu Glu Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys  
 80 85 90  
 ccc gcc tgg gat tct acc atc gag tcg ggg tat ggg gag gcg ccc ccg 459  
 Pro Gly Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro

95		100		105		110	
ccc acg gag agc ctg gaa gca ctc ccc act cct gag gcc tcg ggg ggg							507
Pro Thr Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly							
		115		120		125	
agc ctg gaa atc gat ttt cag gtt gta cag tcg agc agt ttt ggt gga							555
Ser Leu Glu Ile Asp Phe Gln Val Val Gln Ser Ser Ser Phe Gly Gly							
		130		135		140	
gag ggg gcc cta gaa acc tgt agc gca gtg ggg tgg gcg ccc cag agg							603
Glu Gly Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg							
		145		150		155	
tta gtt gac ccg aag agc aag gaa gag gcg atc atc ata gtg gag gat							651
Leu Val Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp							
		160		165		170	
gag gat gag gat gag cgg gag agt atg agg agc agc agg agg cgg cgg							699
Glu Asp Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg							
		175		180		185	190
cgg cgg cgg agg agg aag cag agg aag gtg aag agg gaa agc aga gag							747
Arg Arg Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu							
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aga aat gcc gag agg atg gag agc atc ctg cag gca ctg gag gat att							795
Arg Asn Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile							
		210		215		220	
cag ctg gat ctg gag gca gtg aac atc aag gca ggc aaa gcc ttc ctg							843
Gln Leu Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu							
		225		230		235	
cgt ctc aag cgc aag ttc atc cag atg cga aga ccc ttc ctg gag cgc							891
Arg Leu Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg							
		240		245		250	
aga gac ctc atc atc cag cat atc cca ggc ttc tgg gtc aaa gca ttc							939
Arg Asp Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe							
		255		260		265	270
ctc aac cac ccc aga att tca att ttg atc aac cga cgt gat gaa gac							987
Leu Asn His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp							
		275		280		285	
att ttc cgc tac ttg acc aat ctg cag gta cag gat ctc aga cat atc							1035
Ile Phe Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile							
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tcc atg ggc tac aaa atg aag ctg tac ttc cag act aac ccc tac ttc							1083
Ser Met Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe							
		305		310		315	
aca aac atg gtg att gtc aag gag ttc cag cgc aac cgc tca ggc cgg							1131
Thr Asn Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg							
		320		325		330	
ctg gtg tct cac tca acc cca atc cgc tgg cac cgg ggc cag gaa ccc							1179
Leu Val Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro							
		335		340		345	350
cag gcc cgt cgt cac ggg aac cag gat gcg agc cac agc ttt ttc agc							1227
Gln Ala Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser							
		355		360		365	
tgg ttc tca aac cat agc ctc cca gag gct gac agg att gct gag att							1275
Trp Phe Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile							

370	375	380	
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agg ggc tcc agg ata aag aga aag aag caa gaa atg aag aaa cgt aaa Arg Gly Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys 400 405 410			1371
acc agg ggc aga tgt gag gtg gtg atc atg gaa gac gcc cct gac tat Thr Arg Gly Arg Cys Glu Val Val Ile Met Glu Asp Ala Pro Asp Tyr 415 420 425 430			1419
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att cat gac atc aag atc tct gac ttc atg gag acc acc gac tac ttc Ile His Asp Ile Lys Ile Ser Asp Phe Met Glu Thr Thr Asp Tyr Phe 450 455 460			1515
gag acc act gac aat gag ata act gac atc aat gag aac atc tgc gac Glu Thr Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp 465 470 475			1563
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aac aac gag agt gct gat gac cac gaa acc act gac aac aat gag agt Asn Asn Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser 495 500 505 510			1659
gca gat gac aac aac gag aat cct gaa gac aat aac aag aac act gat Ala Asp Asp Asn Asn Glu Asn Pro Glu Asp Asn Asn Lys Asn Thr Asp 515 520 525			1707
gac aac gaa gag aac cct aac aac aac gag aac act tac ggc aac aac Asp Asn Glu Glu Asn Pro Asn Asn Asn Glu Asn Thr Tyr Gly Asn Asn 530 535 540			1755
ttc ttc aaa ggt ggc ttc tgg ggc agc cat ggc aac aac cag gac agc Phe Phe Lys Gly Gly Phe Trp Gly Ser His Gly Asn Asn Gln Asp Ser 545 550 555			1803
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gtg ata gag atc atc tca gac gaa tca gtg gaa gaa gag ggc att gag Val Ile Glu Ile Ile Ser Asp Glu Ser Val Glu Glu Glu Gly Ile Glu 625 630 635			2043
gaa ggc atc cag caa gat gag gac atc tat gag gaa gga aac tat gag Glu Gly Ile Gln Gln Asp Glu Asp Ile Tyr Glu Glu Gly Asn Tyr Glu			2091

640 645 650

gag gaa gga agt gaa gat gtc tgg gaa gaa ggg gaa gat tcg gac gac 2139  
 Glu Glu Gly Ser Glu Asp Val Trp Glu Glu Gly Glu Asp Ser Asp Asp  
 655 660 665 670

tct gac cta gag gat gtg ctt cag gtc cca aac ggt tgg gcc aat ccg 2187  
 Ser Asp Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro  
 675 680 685

ggg aag agg ggg aaa acc gga taagggtttt ccccttttgg ggatcacctc 2238  
 Gly Lys Arg Gly Lys Thr Gly  
 690

tctgtatccc ccacccaacta tcccatttgc cctctctctc agctagggcc acgcggcccc 2298

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&lt;210&gt; 6

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&lt;212&gt; PRT

&lt;213&gt; NM\_022117 SE20-4

&lt;400&gt; 6

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Pro Leu Leu Arg Leu Pro Leu Pro Pro Pro Gln Gln Arg Pro Arg Leu  
 35 40 45

Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg Gly Val  
 50 55 60

Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Pro Tyr Val Ile Leu Glu  
 65 70 75 80

Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys Pro Gly

85 90 95  
 Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro Pro Thr  
 100 105 110  
 Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly Ser Leu  
 115 120 125  
 Glu Ile Asp Phe Gln Val Val Gln Ser Ser Ser Phe Gly Gly Glu Gly  
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 Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg Leu Val  
 145 150 155 160  
 Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp Glu Asp  
 165 170 175  
 Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg Arg Arg  
 180 185 190  
 Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu Arg Asn  
 195 200 205  
 Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile Gln Leu  
 210 215 220  
 Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu Arg Leu  
 225 230 235 240  
 Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg Arg Asp  
 245 250 255  
 Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe Leu Asn  
 260 265 270  
 His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp Ile Phe  
 275 280 285  
 Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile Ser Met  
 290 295 300  
 Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe Thr Asn  
 305 310 315 320  
 Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg Leu Val  
 325 330 335  
 Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala  
 340 345 350  
 Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser Trp Phe



355                      360                      365  
 Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile Ile Lys  
 370                      375                      380  
 Asn Asp Leu Trp Val Asn Pro Leu Arg Tyr Tyr Leu Arg Glu Arg Gly  
 385                      390                      395                      400  
 Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys Thr Arg  
 405                      410                      415  
 Gly Arg Cys Glu Val Val Ile Met Glu Asp Ala Pro Asp Tyr Tyr Ala  
 420                      425                      430  
 Val Glu Asp Ile Phe Ser Glu Ile Ser Asp Ile Asp Glu Thr Ile His  
 435                      440                      445  
 Asp Ile Lys Ile Ser Asp Phe Met Glu Thr Thr Asp Tyr Phe Glu Thr  
 450                      455                      460  
 Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp Ser Glu  
 465                      470                      475                      480  
 Asn Pro Asp His Asn Glu Val Pro Asn Asn Glu Thr Thr Asp Asn Asn  
 485                      490                      495  
 Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser Ala Asp  
 500                      505                      510  
 Asp Asn Asn Glu Asn Pro Glu Asp Asn Asn Lys Asn Thr Asp Asp Asn  
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 Glu Glu Asn Pro Asn Asn Asn Glu Asn Thr Tyr Gly Asn Asn Phe Phe  
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 Lys Gly Gly Phe Trp Gly Ser His Gly Asn Asn Gln Asp Ser Ser Asp  
 545                      550                      555                      560  
 Ser Asp Asn Glu Ala Asp Glu Ala Ser Asp Asp Glu Asp Asn Asp Gly  
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 Asn Glu Gly Asp Asn Glu Gly Ser Asp Asp Asp Gly Asn Glu Gly Asp  
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 Asn Glu Gly Ser Asp Asp Asp Asp Arg Asp Ile Glu Tyr Tyr Glu Lys  
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 Val Ile Glu Asp Phe Asp Lys Asp Gln Ala Asp Tyr Glu Asp Val Ile  
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 Glu Ile Ile Ser Asp Glu Ser Val Glu Glu Glu Gly Ile Glu Glu Gly

625                      630                      635                      640

Ile Gln Gln Asp Glu Asp Ile Tyr Glu Glu Gly Asn Tyr Glu Glu Glu  
                                 645                                  650                                  655

Gly Ser Glu Asp Val Trp Glu Glu Gly Glu Asp Ser Asp Asp Ser Asp  
                                 660                                  665                                  670

Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro Gly Lys  
                                 675                                  680                                  685

Arg Gly Lys Thr Gly  
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&lt;210&gt; 7

&lt;211&gt; 2632

&lt;212&gt; DNA

&lt;213&gt; NM\_016463 HSPC195

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (931)..(1611)

&lt;223&gt;

&lt;400&gt; 7

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cgcgtcccag cctgcccag cccgcgccc gccatgcgcg ccgcctgctg agtccgggag 180

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									Met	Met	Gly	Gly	5	Ser	Ala	Asp	
									1								
aag	gcc	act	gcg	gct	gca	gcc	gct	gcc	tcc	ctg	ttg	gcc	aat	ggg	cat	1002	
Lys	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Leu	Ala	Asn	Gly	His		
	10					15					20						
gac	ctg	gcg	gcg	gcc	atg	gcg	gtg	gac	aaa	agc	aac	cct	acc	tca	aag	1050	
Asp	Leu	Ala	Ala	Ala	Met	Ala	Val	Asp	Lys	Ser	Asn	Pro	Thr	Ser	Lys		
25					30					35					40		
cac	aaa	agt	ggt	gct	gtg	gcc	agc	ctg	ctg	agc	aag	gca	gag	cgg	gcc	1098	
His	Lys	Ser	Gly	Ala	Val	Ala	Ser	Leu	Leu	Ser	Lys	Ala	Glu	Arg	Ala		
			45						50					55			
acg	gag	ctg	gca	gcc	gag	gga	cag	ctg	acg	ctg	cag	cag	ttt	gcg	cag	1146	
Thr	Glu	Leu	Ala	Ala	Glu	Gly	Gln	Leu	Thr	Leu	Gln	Gln	Phe	Ala	Gln		
			60					65					70				
tcc	aca	gag	atg	ctg	aag	cgc	gtg	gtg	cag	gag	cat	ctc	ccg	ctg	atg	1194	
Ser	Thr	Glu	Met	Leu	Lys	Arg	Val	Val	Gln	Glu	His	Leu	Pro	Leu	Met		
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agc	gag	gcg	ggt	gct	ggc	ctg	cct	gac	atg	gag	gct	gtg	gca	ggt	gcc	1242	
Ser	Glu	Ala	Gly	Ala	Gly	Leu	Pro	Asp	Met	Glu	Ala	Val	Ala	Gly	Ala		
	90				95						100						
gaa	gcc	ctc	aat	ggc	cag	tcc	gac	ttc	ccc	tac	ctg	ggc	gct	ttc	ccc	1290	
Glu	Ala	Leu	Asn	Gly	Gln	Ser	Asp	Phe	Pro	Tyr	Leu	Gly	Ala	Phe	Pro		
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atc	aac	cca	ggc	ctc	ttc	att	atg	acc	ccg	gca	ggt	gtg	ttc	ctg	gcc	1338	
Ile	Asn	Pro	Gly	Leu	Phe	Ile	Met	Thr	Pro	Ala	Gly	Val	Phe	Leu	Ala		
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gag	agc	gcg	ctg	cac	atg	gcg	ggc	ctg	gct	gag	tac	ccc	atg	cag	gga	1386	
Glu	Ser	Ala	Leu	His	Met	Ala	Gly	Leu	Ala	Glu	Tyr	Pro	Met	Gln	Gly		
			140					145					150				
gag	ctg	gcc	tct	gcc	atc	agc	tcc	ggc	aag	aag	aag	cgg	aaa	cgc	tgc	1434	
Glu	Leu	Ala	Ser	Ala	Ile	Ser	Ser	Gly	Lys	Lys	Lys	Arg	Lys	Arg	Cys		
		155					160					165					
ggc	atg	tgc	gcg	ccc	tgc	cgg	cgg	cgc	atc	aac	tgc	gag	cag	tgc	agc	1482	
Gly	Met	Cys	Ala	Pro	Cys	Arg	Arg	Arg	Ile	Asn	Cys	Glu	Gln	Cys	Ser		
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agt	tgt	agg	aat	cga	aag	act	ggc	cat	cag	att	tgc	aaa	ttc	aga	aaa		

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&lt;210&gt; 8

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; NM\_016463 HSPC195

&lt;400&gt; 8

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1          5          10          15

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Ala Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val
20          25          30

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Asp Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser
35          40          45

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Leu Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln
50          55          60

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Leu Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val
65          70          75          80

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Val Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro
85          90          95

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Asp Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp
100          105          110

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Phe Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met  
115 120 125

Thr Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly  
130 135 140

Leu Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser  
145 150 155 160

Gly Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg  
165 170 175

Arg Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly  
180 185 190

His Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro  
195 200 205

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210 215 220

Trp Phe Gln  
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<212> DNA

<213> NM\_017697 FLJ20171

<220>

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<222> (58)..(1131)

<223>

<400> 9

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Met Thr Glu Tyr Leu Asn Phe Glu Lys Ser Ser Ser Val Ser Arg Tyr  
1 5 10 15

gga gcc tct caa gtt gaa gat atg ggg aat ata att tta gca atg att 153  
Gly Ala Ser Gln Val Glu Asp Met Gly Asn Ile Ile Leu Ala Met Ile  
20 25 30

tca gag cct tat aat cac agg ttt tca gat cca gag aga gtg aat tac 201  
Ser Glu Pro Tyr Asn His Arg Phe Ser Asp Pro Glu Arg Val Asn Tyr  
35 40 45

aag ttt gaa agt gga act tgc agc aag atg gaa ctt att gat gat aac Lys Phe Glu Ser Gly Thr Cys Ser Lys Met Glu Leu Ile Asp Asp Asn 50 55 60	249
acc gta gtc agg gca cga ggt tta cca tgg cag tct tca gat caa gat Thr Val Val Arg Ala Arg Gly Leu Pro Trp Gln Ser Ser Asp Gln Asp 65 70 75 80	297
att gca aga ttc ttc aaa gga ctc aat att gcc aag gga ggt gca gca Ile Ala Arg Phe Phe Lys Gly Leu Asn Ile Ala Lys Gly Gly Ala Ala 85 90 95	345
ctt tgt ctg aat gct cag ggt cga agg aac gga gaa gct ctg gtt agg Leu Cys Leu Asn Ala Gln Gly Arg Arg Asn Gly Glu Ala Leu Val Arg 100 105 110	393
ttt gta agt gag gag cac cga gac cta gca cta cag agg cac aaa cat Phe Val Ser Glu Glu His Arg Asp Leu Ala Leu Gln Arg His Lys His 115 120 125	441
cac atg ggg acc cgg tat att gag gtt tac aaa gca aca ggt gaa gat His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp 130 135 140	489
ttc ctt aaa att gct ggt ggt act tcc aat gag gta gcc cag ttt ctc Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu 145 150 155 160	537
tcc aag gaa aat caa gtc att gtt cgc atg cgg ggg ctc cct ttc acg Ser Lys Glu Asn Gln Val Ile Val Arg Met Arg Gly Leu Pro Phe Thr 165 170 175	585
gcc aca gct gaa gaa gtg gtg gcc ttc ttt gga cag cat tgc cct att Ala Thr Ala Glu Glu Val Val Ala Phe Phe Gly Gln His Cys Pro Ile 180 185 190	633
act ggg gga aag gaa ggc atc ctc ttt gtc acc tac cca gat ggt agg Thr Gly Gly Lys Glu Gly Ile Leu Phe Val Thr Tyr Pro Asp Gly Arg 195 200 205	681
cca aca ggg gac gct ttt gtc ctc ttt gcc tgt gag gaa tat gca cag Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu Glu Tyr Ala Gln 210 215 220	729
aat gcg ttg agg aag cat aaa gac ttg ttg ggt aaa aga tac att gaa Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys Arg Tyr Ile Glu 225 230 235 240	777
ctc ttc agg agc aca gca gct gaa gtt cag cag gtg ctg aat cga ttc Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val Leu Asn Arg Phe 245 250 255	825
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ctt cga ggt ctt ccc tat gca gcc aca att gag gac atc ctg gat ttc Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp Ile Leu Asp Phe 290 295 300	969
ctg ggg gag ttc gcc aca gat att cgt act cat ggg gtt cac atg gtt Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly Val His Met Val 305 310 315 320	1017

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ttg aat cac cag ggc cgc cca tca gga gat gcc ttt atc cag atg aag      1065
Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe Ile Gln Met Lys
          325          330          335

tct gcg gac aga gca ttt atg gct gca cag aag tgt cat aaa aaa aaa      1113
Ser Ala Asp Arg Ala Phe Met Ala Ala Gln Lys Cys His Lys Lys Lys
          340          345          350

cat gaa gga cag ata tgt tgaagtcttt cagtgttcag ctgaggagat      1161
His Glu Gly Gln Ile Cys
          355

gaactttgtg ttaatggggg gcactttaaa tcgaaatggc ttatccccac cgccatgtaa      1221

gttaccatgc ctgtctcctc cctcctacac atttcagct cctgctgcag ttattcctac      1281

agaagctgcc atttaccagc cctctgtgat tttgaatcca cgagcactgc agccctccac      1341

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tocacagcct ggcacggtgg tcagaatgca gggcctggcc tacaatactg gagttaagga      1521

aattcttaac ttcttccaag gttaccagtg tttgaaagat gtatggtgat cttgaaacct      1581

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&lt;210&gt; 10

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; NM\_017697 FLJ20171

&lt;400&gt; 10

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Met Thr Glu Tyr Leu Asn Phe Glu Lys Ser Ser Ser Val Ser Arg Tyr
1          5          10          15

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Gly Ala Ser Gln Val Glu Asp Met Gly Asn Ile Ile Leu Ala Met Ile
          20          25          30

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Ser Glu Pro Tyr Asn His Arg Phe Ser Asp Pro Glu Arg Val Asn Tyr  
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 Lys Phe Glu Ser Gly Thr Cys Ser Lys Met Glu Leu Ile Asp Asp Asn  
 50 55 60  
 Thr Val Val Arg Ala Arg Gly Leu Pro Trp Gln Ser Ser Asp Gln Asp  
 65 70 75 80  
 Ile Ala Arg Phe Phe Lys Gly Leu Asn Ile Ala Lys Gly Gly Ala Ala  
 85 90 95  
 Leu Cys Leu Asn Ala Gln Gly Arg Arg Asn Gly Glu Ala Leu Val Arg  
 100 105 110  
 Phe Val Ser Glu Glu His Arg Asp Leu Ala Leu Gln Arg His Lys His  
 115 120 125  
 His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp  
 130 135 140  
 Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu  
 145 150 155 160  
 Ser Lys Glu Asn Gln Val Ile Val Arg Met Arg Gly Leu Pro Phe Thr  
 165 170 175  
 Ala Thr Ala Glu Glu Val Val Ala Phe Phe Gly Gln His Cys Pro Ile  
 180 185 190  
 Thr Gly Gly Lys Glu Gly Ile Leu Phe Val Thr Tyr Pro Asp Gly Arg  
 195 200 205  
 Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu Glu Tyr Ala Gln  
 210 215 220  
 Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys Arg Tyr Ile Glu  
 225 230 235 240  
 Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val Leu Asn Arg Phe  
 245 250 255  
 Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro Ile Ile Pro Val  
 260 265 270  
 Leu Pro Gln Gln Phe Val Pro Pro Thr Asn Val Arg Asp Cys Ile Arg  
 275 280 285  
 Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp Ile Leu Asp Phe  
 290 295 300



Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly Val His Met Val  
 305 310 315 320

Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe Ile Gln Met Lys  
 325 330 335

Ser Ala Asp Arg Ala Phe Met Ala Ala Gln Lys Cys His Lys Lys Lys  
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His Glu Gly Gln Ile Cys  
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<212> DNA

<213> NM\_052886 MAL2

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 Met Ser Ala Gly Gly Ala Ser Val Pro Pro Pro  
 1 5 10

ccg aac ccc gcc gtg tcc ttc ccg ccg ccc cgg gtc acc ctg ccc gcc 160  
 Pro Asn Pro Ala Val Ser Phe Pro Pro Pro Arg Val Thr Leu Pro Ala  
 15 20 25

ggc ccc gac atc ctg cgg acc tac tcg gcc gcc ttc gtc tgc ctg gag 208  
 Gly Pro Asp Ile Leu Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu  
 30 35 40

att ctg ttc ggg ggt ctt gtc tgg att ttg gtt gcc tcc tcc aat gtt 256  
 Ile Leu Phe Gly Gly Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val  
 45 50 55

cct cta cct cta cta caa gga tgg gtc atg ttt gtg tcc gtg aca gcg 304  
 Pro Leu Pro Leu Leu Gln Gly Trp Val Met Phe Val Ser Val Thr Ala  
 60 65 70 75

ttt ttc ttt tcg ctc ctc ttt ctg ggc atg ttc ctc tct ggc atg gtg 352  
 Phe Phe Phe Ser Leu Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val  
 80 85 90

gct caa att gat gct aac tgg aac ttc ctg gat ttt gcc tac cat ttt 400  
 Ala Gln Ile Asp Ala Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe  
 95 100 105

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Thr Val Phe Val Phe Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala	
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Thr Ser Leu His Asp Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro	
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ctc ctg agt gat aac cag tat aac ata aac gta gca gcc tca att ttt	544
Leu Leu Ser Asp Asn Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe	
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Arg Arg Trp Arg Pro	
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<211> 176

<212> PRT

<213> NM\_052886 MAL2

<400> 12

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Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu Ile Leu Phe Gly Gly  
35 40 45

Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val Pro Leu Pro Leu Leu  
50 55 60

Gln Gly Trp Val Met Phe Val Ser Val Thr Ala Phe Phe Phe Ser Leu  
65 70 75 80

Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala  
85 90 95

Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe  
100 105 110

Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp

115 120 125

Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro Leu Leu Ser Asp Asn  
130 135 140

Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr  
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Met Pro Arg Pro Glu Leu Pro Leu Pro Glu Gly Trp Glu Glu  
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gcg cgc gac ttc gac ggc aag gtc tac tac ata gac cac acg aac cgc 156  
Ala Arg Asp Phe Asp Gly Lys Val Tyr Tyr Ile Asp His Thr Asn Arg  
15 20 25 30

acc acc agc tgg atc gac ccg cgg gac agg tac acc aaa ccg ctc acc 204  
Thr Thr Ser Trp Ile Asp Pro Arg Asp Arg Tyr Thr Lys Pro Leu Thr  
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ttt gct gac tgc att agt gat gag ttg ccg cta gga tgg gaa gag gca 252  
Phe Ala Asp Cys Ile Ser Asp Glu Leu Pro Leu Gly Trp Glu Glu Ala  
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tat gac cca cag gtt gga gat tac ttc ata gac cac aac acc aaa acc 300  
Tyr Asp Pro Gln Val Gly Asp Tyr Phe Ile Asp His Asn Thr Lys Thr  
65 70 75

act cag att gag gat cct cga gta caa tgg cgg cgg gag cag gaa cat 348  
Thr Gln Ile Glu Asp Pro Arg Val Gln Trp Arg Arg Glu Gln Glu His  
80 85 90

atg ctg aag gat tac ctg gtg gtg gcc cag gag gct ctg agt gca caa 396  
Met Leu Lys Asp Tyr Leu Val Val Ala Gln Glu Ala Leu Ser Ala Gln  
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aag gag atc tac cag gtg aag cag cag cgc ctg gag ctt gca cag cag 444

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Glu	Tyr	Gln	Gln	Leu	His	Ala	Val	Trp	Glu	His	Lys	Leu	Gly	Ser	Gln	
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Val	Ser	Leu	Val	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Lys	Tyr	Asp	Pro	Glu	
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Lys	Arg	Glu	Met	Val	His	Leu	Gln	His	Glu	Leu	Gln	Phe	Lys	Glu	Arg	
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Ala	Ile	Lys	Lys	Ala	Ile	Thr	Cys	Gly	Glu	Lys	Glu	Lys	Gln	Asp	Leu	
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Ile	Lys	Ser	Leu	Ala	Met	Leu	Lys	Asp	Gly	Phe	Arg	Thr	Asp	Arg	Gly	
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Phe	Pro	Leu	Pro	Lys	Gln	Tyr	Leu	Asp	Val	Ser	Ser	Gln	Thr	Asp	Ile	
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Ser	Gly	Ser	Phe	Gly	Ile	Asn	Ser	Asn	Asn	Gln	Leu	Ala	Glu	Lys	Val	
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Arg	Leu	Arg	Leu	Arg	Tyr	Glu	Glu	Ala	Lys	Arg	Arg	Ile	Ala	Asn	Leu	
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Leu	Lys	Glu	Met	Arg	Phe	Ile	Ser	Pro	Arg	Lys	Trp	Thr	Gln	Gly	Glu	
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Val	Glu	Gln	Leu	Glu	Met	Ala	Arg	Lys	Arg	Leu	Glu	Lys	Asp	Leu	Gln	
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Asp Cys Ile Ser Asp Glu Leu Pro Leu Gly Trp Glu Glu Ala Tyr Asp  
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Pro Gln Val Gly Asp Tyr Phe Ile Asp His Asn Thr Lys Thr Thr Gln  
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Ile Glu Asp Pro Arg Val Gln Trp Arg Arg Glu Gln Glu His Met Leu  
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Lys Asp Tyr Leu Val Val Ala Gln Glu Ala Leu Ser Ala Gln Lys Glu  
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Gln Gln Leu His Ala Val Trp Glu His Lys Leu Gly Ser Gln Val Ser  
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170

175

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Tyr Lys Leu Asp Glu Ala Gln Ala Val Leu Arg Glu Thr Lys Ala Ile  
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Lys Lys Ala Ile Thr Cys Gly Glu Lys Glu Lys Gln Asp Leu Ile Lys  
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Gln Gly Cys Gly Leu Lys Val Ala Cys Val Ser Ala Ala Val Ser Asp  
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Lys Gln Phe Ala Ile Leu Ile Ile Gln Leu Ser Asn Leu Ser Ala Leu  
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Ser Asp Thr Leu Val Phe Asn Glu Val Phe Trp Val Ser Met Ser Tyr  
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Pro Ala Leu His Gln Lys Thr Leu Arg Val Asp Val Cys Thr Thr Asp  
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Glu Val Cys Arg Ser Gly Glu Arg Ser Thr Arg Trp Tyr Asn Leu Leu  
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785 790 795 800

Val Met Ala Pro Ala Ser Gly Pro Ala Ser Thr Asp Ala Val Ser Ala  
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Ser Ser Thr Gln Thr Leu Glu Asp Ser Trp Arg Tyr Glu Glu Thr Ser  
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Glu Asn Glu Ala Val Ala Glu Glu Glu Glu Glu Val Glu Glu Glu  
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Glu Gly Glu Glu Asp Val Phe Thr Glu Lys Ala Ser Pro Asp Met Asp  
865 870 875 880

Gly Tyr Pro Ala Leu Lys Val Asp Lys Glu Thr Asn Thr Glu Thr Pro  
885 890 895

Ala Pro Ser Pro Thr Val Val Arg Pro Lys Asp Arg Arg Val Gly Thr  
900 905 910

Pro Ser Gln Gly Pro Phe Leu Arg Gly Ser Thr Ile Ile Arg Ser Lys  
915 920 925

Thr Phe Ser Pro Gly Pro Gln Ser Gln Tyr Val Cys Arg Leu Asn Arg  
930 935 940

Ser Asp Ser Asp Ser Ser Thr Leu Ser Lys Lys Pro Pro Phe Val Arg  
945 950 955 960

Asn Ser Leu Glu Arg Arg Ser Val Arg Met Lys Arg Pro Ser Ser Val  
965 970 975

Lys Ser Leu Arg Ser Glu Arg Leu Ile Arg Thr Ser Leu Asp Leu Glu  
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Ile Ser Val Leu Lys Glu Leu Lys Glu Gln Leu Glu Gln Ala Lys  
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Ser His Gly Glu Lys Glu Leu Pro Gln Trp Leu Arg Glu Asp Glu  
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Arg Phe Arg Leu Leu Leu Arg Met Leu Glu Lys Arg Gln Met Asp  
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Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys  
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Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg  
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Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val  
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Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala  
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Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala  
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Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg  
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Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly  
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Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly  
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Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr  
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Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala  
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Trp Lys Ala Leu Thr Leu Ala Glu Lys Arg Pro Phe Val Glu Glu Ala
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gag ccg ctg cgc gtg cag cac atg cag gac cac ccc aac tac aag tac 615
Glu Arg Leu Arg Val Gln His Met Gln Asp His Pro Asn Tyr Lys Tyr
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Pro Ala Asn Ser Gly Ala Pro Ala Gly Ala Ala Gly Arg Ala Lys Gly  
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Glu Ser Arg Ile Arg Arg Pro Met Asn Ala Phe Met Val Trp Ala Lys  
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Asp Glu Arg Lys Arg Leu Ala Gln Gln Asn Pro Asp Leu His Asn Ala  
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Glu Leu Ser Lys Met Leu Gly Lys Ser Trp Lys Ala Leu Thr Leu Ala  
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Glu Lys Arg Pro Phe Val Glu Glu Ala Glu Arg Leu Arg Val Gln His  
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Met Gln Asp His Pro Asn Tyr Lys Tyr Arg Pro Arg Arg Arg Lys Gln  
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Glu Pro Gln Ala Ala Ala Leu Gly Pro Glu Gly Gly Arg Val Ala Met  
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Asp Gly Leu Gly Leu Gln Phe Pro Glu Gln Gly Phe Pro Ala Gly Pro  
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Pro Leu Leu Pro Pro His Met Gly Gly His Tyr Arg Asp Cys Gln Ser  
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Ser Asp Tyr Ala Gly Pro Pro Glu Pro Pro Ala Gly Pro Met His Pro  
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Arg Leu Gly Pro Glu Pro Ala Gly Pro Ser Ile Pro Gly Leu Leu Ala  
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Pro Pro Ser Ala Leu His Val Tyr Tyr Gly Ala Met Gly Ser Pro Gly  
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His Gln His Gln His His Pro Pro Gly Pro Gly Gln Pro Ser Pro Pro  
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Leu	Arg	Pro	His	Thr	Gln	Lys	Trp	Ser	His	Val	Leu	Thr	Leu	Leu	Gly	
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Ala	Ser	Gly	Thr	Phe	Gln	Leu	Val	Val	Leu	Tyr	Leu	Phe	Ser	Ile	Ile	
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acc	tcc	ttc	caa	ggc	ttc	ctc	atc	ttc	atc	tgg	tac	tgg	tcc	atg	cgg	2144
Thr	Ser	Phe	Gln	Gly	Phe	Leu	Ile	Phe	Ile	Trp	Tyr	Trp	Ser	Met	Arg	
			650					655					660			
ctg	cag	gcc	cgg	ggg	ggc	ccc	tcc	cct	ctg	aag	agc	aac	tca	gac	agc	2192
Leu	Gln	Ala	Arg	Gly	Gly	Pro	Ser	Pro	Leu	Lys	Ser	Asn	Ser	Asp	Ser	
		665				670						675				
gcc	agg	ctc	ccc	atc	agc	tcg	ggc	agc	acc	tcg	tcc	agc	cgc	atc		2237
Ala	Arg	Leu	Pro	Ile	Ser	Ser	Gly	Ser	Thr	Ser	Ser	Ser	Arg	Ile		
		680				685					690					
taaggcctcca	gcccacctgc	ccatgtgatg	aagcagaqat	gcgcctcgt	cgcacactgc											2297

ctgtggcccc cgagccaggc ccagccccag gccagtcagc cgcagacttt ggaaagccca 2357  
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 ccaccactcc aaggactgag actgacctcc totggtgaca ctggcctaga gcctgacact 3257  
 ctctaaagag gttctctcca agccccaaa tagctccagg cgccctcggc cgcccatcat 3317  
 ggttaattct gtccaacaaa cacacacggg tagattgctg gcctgttgta ggtggtaggg 3377  
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 ctttttacgt accaattctt ttgtctttt atattaaaaa gaagtacatg ttcattgtag 3617  
 agaatttgga aactgtagaa gagaatcaag aagaaaaata aaaatcagct gttgtaatcg 3677  
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&lt;210&gt; 20

&lt;211&gt; 693

&lt;212&gt; PRT

&lt;213&gt; NM\_005682 GPR56

&lt;400&gt; 20

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu  
 1 5 10 15

Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe

20	25	30
Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr 35 40 45		
Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala 50 55 60		
Leu Thr Val His Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser 65 70 75 80		
Phe Pro Asp Pro Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg 85 90 95		
His Ala Gly Arg Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu 100 105 110		
Ser Asp Lys Ala Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser 115 120 125		
Leu Ala Gln Gly Pro Pro Leu Leu Ala Thr Ser Val Thr Ser Trp Trp 130 135 140		
Ser Pro Gln Asn Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser 145 150 155 160		
Phe His Ser Pro Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met 165 170 175		
Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His 180 185 190		
Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln 195 200 205		
Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp 210 215 220		
Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu 225 230 235 240		
Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu 245 250 255		
Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr 260 265 270		
Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu 275 280 285		
Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser		



290

295

300

Ser His Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr  
 305 310 315 320

Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln  
 325 330 335

Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp  
 340 345 350

Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr  
 355 360 365

Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr Tyr  
 370 375 380

Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His Lys  
 385 390 395 400

His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu  
 405 410 415

Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu  
 420 425 430

Pro Cys Arg Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn  
 435 440 445

Leu Leu Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu  
 450 455 460

Pro Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile  
 465 470 475 480

Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu  
 485 490 495

Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val  
 500 505 510

Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile  
 515 520 525

Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp Asn Tyr Gly Pro  
 530 535 540

Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser  
 545 550 555 560

Met Cys Trp Ile Arg Asp Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly  
565 570 575

Leu Phe Ser Leu Val Phe Leu Phe Asn Met Ala Met Leu Ala Thr Met  
580 585 590

Val Val Gln Ile Leu Arg Leu Arg Pro His Thr Gln Lys Trp Ser His  
595 600 605

Val Leu Thr Leu Leu Gly Leu Ser Leu Val Leu Gly Leu Pro Trp Ala  
610 615 620

Leu Ile Phe Phe Ser Phe Ala Ser Gly Thr Phe Gln Leu Val Val Leu  
625 630 635 640

Tyr Leu Phe Ser Ile Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile  
645 650 655

Trp Tyr Trp Ser Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu  
660 665 670

Lys Ser Asn Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr  
675 680 685

Ser Ser Ser Arg Ile  
690

<210> 21

<211> 1332

<212> DNA

<213> NM\_001307 claudin 7, CLDN7

<220>

<221> CDS

<222> (427)..(1059)

<223>

<400> 21

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tgcctagggg cgccgagagc gcccgagggg aaccgcctgg ccttcgggga ccaccaattt	180
tgtctggaac caccctcccg gcgtatccta ctccctgtgc cgcgaggcca tcgcttcact	240
ggaggggtcg atttgtgtgt agtttggtga caagatttgc attcacctgg cccaaaccct	300
ttttgtctct ttgggtgacc ggaaaactcc acctcaagtt ttcttttgtg gggtgcccc	360

ccaagtgtcg tttgttttac tgtagggctc cccgcccgcc gcccccagtg ttttctgagg 420

gcggaa atg gcc aat tgc gcc ctg cag ttg ctg gcc ttc tcc atg gcc 468  
Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser Met Ala  
1 5 10

ctg ctg gcc tgg gtg ggt ctg gtg gcc tgc acc gcc atc ccg cag tgg 516  
Leu Leu Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp  
15 20 25 30

cag atg agc tcc tat gcg ggt gac aac atc atc acg gcc cag gcc atg 564  
Gln Met Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met  
35 40 45

tac aag ggg ctg tgg atg gac tgc gtc acg cag agc acg ggg atg atg 612  
Tyr Lys Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met  
50 55 60

agc tgc aaa atg tac gac tgc gtg ctc gcc ctg tcc gcg gcc ttg cag 660  
Ser Cys Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln  
65 70 75

gcc act cga gcc cta atg gtg gtc tcc ctg gtg ctg gcc ttc ctg gcc 708  
Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala  
80 85 90

atg ttt gtg gcc acg atg ggc atg aag tgc acg cgc tgt ggg gga gac 756  
Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp  
95 100 105 110

gac aaa gtg aag aag gcc cgt ata gcc atg ggt gga gcc ata att ttc 804  
Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe  
115 120 125

atc gtg gca ggt ctt gcc acc ttg gta gct tgc tcc tgg tat gcc cat 852  
Ile Val Ala Gly Leu Ala Thr Leu Val Ala Cys Ser Trp Tyr Gly His  
130 135 140

cag att gtc aca gac ttt tat aac cct ttg atc cct acc aac att aag 900  
Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys  
145 150 155

tat gag ttt gcc cct gcc atc ttt att ggc tgg gca ggg tct gcc cta 948  
Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu  
160 165 170

gtc atc ctg gga ggt gca ctg ctc tcc tgt tcc tgt cct ggg aat gag 996  
Val Ile Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu  
175 180 185 190

agc aag gct ggg tac cgt gca ccc cgc tct tac cct aag tcc aac tct 1044  
Ser Lys Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser  
195 200 205

tcc aag gag tat gtg tgacctggga tctccttgcc ccagcctgac aggctatggg 1099  
Ser Lys Glu Tyr Val  
210

agtgtctaga tgcctgaaag ggcctggggc tgagctcagc ctgtgggcag ggtgccggac 1159

aaaggcctcc tggtcactct gtccctgcac tccatgtata gtcctcttggt gttgggggtg 1219

gggggggtgcc gttggtggga gagacaaaaa gagggagagt gtgctttttg tacagtaata 1279

aaaaataagt attgggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1332

&lt;210&gt; 22

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; NM\_001307 claudin 7, CLDN7

&lt;400&gt; 22

Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser Met Ala Leu Leu  
 1 5 10 15

Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp Gln Met  
 20 25 30

Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met Tyr Lys  
 35 40 45

Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys  
 50 55 60

Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr  
 65 70 75 80

Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe  
 85 90 95

Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys  
 100 105 110

Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe Ile Val  
 115 120 125

Ala Gly Leu Ala Thr Leu Val Ala Cys Ser Trp Tyr Gly His Gln Ile  
 130 135 140

Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu  
 145 150 155 160

Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu Val Ile  
 165 170 175

Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys  
 180 185 190

Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser Ser Lys  
 195 200 205

Glu Tyr Val  
 210

&lt;210&gt; 23

&lt;211&gt; 888

&lt;212&gt; DNA

&lt;213&gt; NM\_014736 KIAA0101 gene product

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (75)..(407)

&lt;223&gt;

&lt;400&gt; 23

ggggccttgt ccagtgaac accctcggct gggaagtcag ttctgttctct cctctcctct 60

cttcttgttt gaac atg gtg cgg act aaa gca gac agt gtt cca ggc act 110  
 Met Val Arg Thr Lys Ala Asp Ser Val Pro Gly Thr  
 1 5 10

tac aga aaa gtg gtg gct gct cga gcc ccc aga aag gtg ctt ggt tct 158  
 Tyr Arg Lys Val Val Ala Ala Arg Ala Pro Arg Lys Val Leu Gly Ser  
 15 20 25

tcc acc tct gcc act aat tcg aca tca gtt tca tcg agg aaa gct gaa 206  
 Ser Thr Ser Ala Thr Asn Ser Thr Ser Val Ser Arg Lys Ala Glu  
 30 35 40

aat aaa tat gca gga ggg aac ccc gtt tgc gtg cgc cca act ccc aag 254  
 Asn Lys Tyr Ala Gly Gly Asn Pro Val Cys Val Arg Pro Thr Pro Lys  
 45 50 55 60

tgg caa aaa gga att gga gaa ttc ttt agg ttg tcc cct aaa gat tct 302  
 Trp Gln Lys Gly Ile Gly Glu Phe Phe Arg Leu Ser Pro Lys Asp Ser  
 65 70 75

gaa aaa gag aat cag att cct gaa gag gca gga agc agt ggc tta gga 350  
 Glu Lys Glu Asn Gln Ile Pro Glu Glu Ala Gly Ser Ser Gly Leu Gly  
 80 85 90

aaa gca aag aga aaa gca tgt cct ttg caa cct gat cac aca aat gat 398  
 Lys Ala Lys Arg Lys Ala Cys Pro Leu Gln Pro Asp His Thr Asn Asp  
 95 100 105

gaa aaa gaa tagaactttc tcattcatct ttgaataacg tctccttggt 447  
 Glu Lys Glu  
 110

taccctggta ttctagaatg taaattttaca taaatgtgtt tgttccaatt agctttgttg 507

aacaggcatt taattaaaaa atttaggttt aaatttagat gttcaaaagt agttgtgaaa 567

tttgagaatt tgtaagacta attatggtaa cttagcttag tattcaatat aatgcattgt 627

ttgggttctt ttaccaaatt aagtgtctag ttcttgctaa aatcaagtca ttgcattgtg 687

ttctaattac aagtatgttg tatttgagat ttgcttagat tgttgtactg ctgccatttt 747

tattggtggt tgattattgg aatggtgcc aattgtcact ccttctactt gctttaaaaa 807

gcagagttag atttttgcac attaaaaaaa ttcagtatta attaaacact aaaaaaaaaa 867

58

aaaaaaaaa aaaaaaaaaa a

888

&lt;210&gt; 24

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; NM\_014736 KIAA0101 gene product

&lt;400&gt; 24

Met Val Arg Thr Lys Ala Asp Ser Val Pro Gly Thr Tyr Arg Lys Val  
 1 5 10 15

Val Ala Ala Arg Ala Pro Arg Lys Val Leu Gly Ser Ser Thr Ser Ala  
 20 25 30

Thr Asn Ser Thr Ser Val Ser Ser Arg Lys Ala Glu Asn Lys Tyr Ala  
 35 40 45

Gly Gly Asn Pro Val Cys Val Arg Pro Thr Pro Lys Trp Gln Lys Gly  
 50 55 60

Ile Gly Glu Phe Phe Arg Leu Ser Pro Lys Asp Ser Glu Lys Glu Asn  
 65 70 75 80

Gln Ile Pro Glu Glu Ala Gly Ser Ser Gly Leu Gly Lys Ala Lys Arg  
 85 90 95

Lys Ala Cys Pro Leu Gln Pro Asp His Thr Asn Asp Glu Lys Glu  
 100 105 110

&lt;210&gt; 25

&lt;211&gt; 598

&lt;212&gt; DNA

&lt;213&gt; NM\_003064 secretory leukocyte protease inhibitor, SLPI

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (23)..(418)

&lt;223&gt;

&lt;400&gt; 25

cagagtcact cctgccttca cc atg aag tcc agc ggc ctc ttc ccg ttc ctg  
 Met Lys Ser Ser Gly Leu Phe Pro Phe Leu  
 1 5 10

52

gtg ctg ctt gcc ctg gga act ctg gca cct tgg gct gtg gaa ggc tct 100  
Val Leu Leu Ala Leu Gly Thr Leu Ala Pro Trp Ala Val Glu Gly Ser  
15 20 25

gga aag tcc ttc aaa gct gga gtc tgt cct cct aag aaa tct gcc cag 148  
Gly Lys Ser Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala Gln  
30 35 40

tgc ctt aga tac aag aaa cct gag tgc cag agt gac tgg cag tgt cca 196  
Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro  
45 50 55

ggg aag aag aga tgt tgt cct gac act tgt ggc atc aaa tgc ctg gat 244  
Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp  
60 65 70

cct gtt gac acc cca aac cca aca agg agg aag cct ggg aag tgc cca 292  
Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro  
75 80 85 90

gtg act tat ggc caa tgt ttg atg ctt aac ccc ccc aat ttc tgt gag 340  
Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu  
95 100 105

atg gat ggc cag tgc aag cgt gac ttg aag tgt tgc atg ggc atg tgt 388  
Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met Cys  
110 115 120

ggg aaa tcc tgc gtt tcc cct gtg aaa gct tgattcctgc catatggagg 438  
Gly Lys Ser Cys Val Ser Pro Val Lys Ala  
125 130

aggctctgga gtccgtctct gtgtggtcca ggtcctttcc accctgagac ttggctccac 498

cactgatatc ctcccttggg gaaaggcttg gcacacagca ggctttcaag aagtgccagt 558

tgatcaatga ataaataaac gagcctatct ctctttgcac 598

&lt;210&gt; 26

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; NM\_003064 secretory leukocyte protease inhibitor, SLPI

&lt;400&gt; 26

Met Lys Ser Ser Gly Leu Phe Pro Phe Leu Val Leu Leu Ala Leu Gly  
1 5 10 15

Thr Leu Ala Pro Trp Ala Val Glu Gly Ser Gly Lys Ser Phe Lys Ala  
20 25 30

Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys  
35 40 45

Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys  
50 55 60

Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn  
65 70 75 80

Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys  
85 90 95

Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys  
100 105 110

Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser  
115 120 125

Pro Val Lys Ala  
130

<210> 27

<211> 3970

<212> DNA

<213> NM\_013994 DDR1

<220>

<221> CDS

<222> (337)..(3093)

<223>

<400> 27  
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ggccagtgtc tggcacaggg gaagcattct aaaaatatag ctgatgctgt taaacaatga 180  
ctgttggtgt tgttttactg ttattatccc caaagcggcc cattctgtct gttgctgtca 240  
gctatgactc agtcccctga ttaacttacg caccacccat tttatcccct gcagagatgc 300  
tgccccacc cccttaggcc cgagggatca ggagct atg gga cca gag gcc ctg 354  
Met Gly Pro Glu Ala Leu  
1 5  
tca tct tta ctg ctg ctg ctc ttg gtg gca agt gga gat gct gac atg 402  
Ser Ser Leu Leu Leu Leu Leu Val Ala Ser Gly Asp Ala Asp Met  
10 15 20  
aag gga cat ttt gat cct gcc aag tgc cgc tat gcc ctg ggc atg cag 450  
Lys Gly His Phe Asp Pro Ala Lys Cys Arg Tyr Ala Leu Gly Met Gln  
25 30 35  
gac cgg acc atc cca gac agt gac atc tct gct tcc agc tcc tgg tca 498  
Asp Arg Thr Ile Pro Asp Ser Asp Ile Ser Ala Ser Ser Ser Trp Ser  
40 45 50  
gat tcc act gcc gcc cgc cac agc agg ttg gag agc agt gac ggg gat 546



Asp 55	Ser	Thr	Ala	Ala	Arg	His	Ser	Arg	Leu	Glu	Ser	Ser	Asp	Gly	Asp 70	
					60					65						
ggg	gcc	tgg	tgc	ccc	gca	ggg	tcg	gtg	ttt	ccc	aag	gag	gag	gag	tac	594
Gly	Ala	Trp	Cys	Pro	Ala	Gly	Ser	Val	Phe	Pro	Lys	Glu	Glu	Glu	Tyr	
				75					80					85		
ttg	cag	gtg	gat	cta	caa	cga	ctg	cac	ctg	gtg	gct	ctg	gtg	ggc	acc	642
Leu	Gln	Val	Asp	Leu	Gln	Arg	Leu	His	Leu	Val	Ala	Leu	Val	Gly	Thr	
			90					95					100			
cag	gga	cgg	cat	gcc	ggg	ggc	ctg	ggc	aag	gag	ttc	tcc	cgg	agc	tac	690
Gln	Gly	Arg	His	Ala	Gly	Gly	Leu	Gly	Lys	Glu	Phe	Ser	Arg	Ser	Tyr	
		105					110					115				
cgg	ctg	cgt	tac	tcc	cgg	gat	ggg	cgc	cgc	tgg	atg	ggc	tgg	aag	gac	738
Arg	Leu	Arg	Tyr	Ser	Arg	Asp	Gly	Arg	Arg	Trp	Met	Gly	Trp	Lys	Asp	
	120					125					130					
cgc	tgg	ggt	cag	gag	gtg	atc	tca	ggc	aat	gag	gac	cct	gag	gga	gtg	786
Arg	Trp	Gly	Gln	Glu	Val	Ile	Ser	Gly	Asn	Glu	Asp	Pro	Glu	Gly	Val	
135					140					145					150	
gtg	ctg	aag	gac	ctt	ggg	ccc	ccc	atg	gtt	gcc	cga	ctg	gtt	cgc	ttc	834
Val	Leu	Lys	Asp	Leu	Gly	Pro	Pro	Met	Val	Ala	Arg	Leu	Val	Arg	Phe	
				155				160						165		
tac	ccc	cgg	gct	gac	cgg	gtc	atg	agc	gtc	tgt	ctg	cgg	gta	gag	ctc	882
Tyr	Pro	Arg	Ala	Asp	Arg	Val	Met	Ser	Val	Cys	Leu	Arg	Val	Glu	Leu	
			170				175						180			
tat	ggc	tgc	ctc	tgg	agg	gat	gga	ctc	ctg	tct	tac	acc	gcc	cct	gtg	930
Tyr	Gly	Cys	Leu	Trp	Arg	Asp	Gly	Leu	Leu	Ser	Tyr	Thr	Ala	Pro	Val	
		185					190					195				
ggg	cag	aca	atg	tat	tta	tct	gag	gcc	gtg	tac	ctc	aac	gac	tcc	acc	978
Gly	Gln	Thr	Met	Tyr	Leu	Ser	Glu	Ala	Val	Tyr	Leu	Asn	Asp	Ser	Thr	
	200					205					210					
tat	gac	gga	cat	acc	gtg	ggc	gga	ctg	cag	tat	ggg	ggt	ctg	ggc	cag	1026
Tyr	Asp	Gly	His	Thr	Val	Gly	Gly	Leu	Gln	Tyr	Gly	Gly	Leu	Gly	Gln	
215					220					225					230	
ctg	gca	gat	ggt	gtg	gtg	ggg	ctg	gat	gac	ttt	agg	aag	agt	cag	gag	1074
Leu	Ala	Asp	Gly	Val	Val	Gly	Leu	Asp	Asp	Phe	Arg	Lys	Ser	Gln	Glu	
				235					240					245		
ctg	cgg	gtc	tgg	cca	ggc	tat	gac	tat	gtg	gga	tgg	agc	aac	cac	agc	1122
Leu	Arg	Val	Trp	Pro	Gly	Tyr	Asp	Tyr	Val	Gly	Trp	Ser	Asn	His	Ser	
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ttc	tcc	agt	ggc	tat	gtg	gag	atg	gag	ttt	gag	ttt	gac	cgg	ctg	agg	1170
Phe	Ser	Ser	Gly	Tyr	Val	Glu	Met	Glu	Phe	Glu	Phe	Asp	Arg	Leu	Arg	
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gcc	ttc	cag	gct	atg	cag	gtc	cac	tgt	aac	aac	atg	cac	acg	ctg	gga	1218
Ala	Phe	Gln	Ala	Met	Gln	Val	His	Cys	Asn	Asn	Met	His	Thr	Leu	Gly	
	280					285					290					
gcc	cgt	ctg	cct	ggc	ggg	gtg	gaa	tgt	cgc	ttc	cgg	cgt	ggc	cct	gcc	1266
Ala	Arg	Leu	Pro	Gly	Gly	Val	Glu	Cys	Arg	Phe	Arg	Arg	Gly	Pro	Ala	
295					300					305					310	
atg	gcc	tgg	gag	ggg	gag	ccc	atg	cgc	cac	aac	cta	ggg	ggc	aac	ctg	1314
Met	Ala	Trp	Glu	Gly	Glu	Pro	Met	Arg	His	Asn	Leu	Gly	Gly	Asn	Leu	
				315					320					325		

ggg gac ccc aga gcc cgg gct gtc tca gtg ccc ctt ggc ggc cgt gtg Gly Asp Pro Arg Ala Arg Ala Val Ser Val Pro Leu Gly Gly Arg Val 330 335 340	1362
gct cgc ttt ctg cag tgc cgc ttc ctc ttt gcg ggg ccc tgg tta ctc Ala Arg Phe Leu Gln Cys Arg Phe Leu Phe Ala Gly Pro Trp Leu Leu 345 350 355	1410
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cct ccc acc aac ttc agc agc ttg gag ctg gag ccc aga ggc cag cag Pro Pro Thr Asn Phe Ser Ser Leu Glu Leu Glu Pro Arg Gly Gln Gln 395 400 405	1554
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act tac gcc cgt ccc cct cga ggc ccg ggc ccc ccc aca ccc gcc tgg Thr Tyr Ala Arg Pro Pro Arg Gly Pro Gly Pro Pro Thr Pro Ala Trp 520 525 530	1938
gcc aaa ccc acc aac acc cag gcc tac agt ggg gac tat atg gag cct Ala Lys Pro Thr Asn Thr Gln Ala Tyr Ser Gly Asp Tyr Met Glu Pro 535 540 545 550	1986
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gag aac ggc gac ctc aac cag ttc ctc agt gcc cac cag ctg gag gac Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser Ala His Gln Leu Glu Asp 715 720 725	2514
aag gca gcc gag ggg gcc cct ggg gac ggg cag gct gcg cag ggg ccc Lys Ala Ala Glu Gly Ala Pro Gly Asp Gly Gln Ala Ala Gln Gly Pro 730 735 740	2562
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His Arg Arg Ala Gly	His Arg Glu Arg Gly	Gly Val Leu Pro Gly Pro	
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Pro Phe Ser Gln Leu His Arg Phe Leu Ala Glu Asp Ala Leu Asn Thr			
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Glu Ser Ser Asp Gly Asp Gly Ala Trp Cys Pro Ala Gly Ser Val Phe		
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Pro Lys Glu Glu Glu Tyr Leu Gln Val Asp Leu Gln Arg Leu His Leu		
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Val Ala Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly Leu Gly Lys		
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Glu Phe Ser Arg Ser Tyr Arg Leu Arg Tyr Ser Arg Asp Gly Arg Arg		
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Trp Met Gly Trp Lys Asp Arg Trp Gly Gln Glu Val Ile Ser Gly Asn		
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Glu Asp Pro Glu Gly Val Val Leu Lys Asp Leu Gly Pro Pro Met Val		
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Cys Leu Arg Val Glu Leu Tyr Gly Cys Leu Trp Arg Asp Gly Leu Leu		
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Ser Tyr Thr Ala Pro Val Gly Gln Thr Met Tyr Leu Ser Glu Ala Val		
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Tyr Leu Asn Asp Ser Thr Tyr Asp Gly His Thr Val Gly Gly Leu Gln		
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Tyr Gly Gly Leu Gly Gln Leu Ala Asp Gly Val Val Gly Leu Asp Asp		
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Phe Arg Lys Ser Gln Glu Leu Arg Val Trp Pro Gly Tyr Asp Tyr Val		
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Gly Trp Ser Asn His Ser Phe Ser Ser Gly Tyr Val Glu Met Glu Phe		
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Glu Phe Asp Arg Leu Arg Ala Phe Gln Ala Met Gln Val His Cys Asn		
	275	280
Asn Met His Thr Leu Gly Ala Arg Leu Pro Gly Gly Val Glu Cys Arg		

290                      295                      300  
 Phe Arg Arg Gly Pro Ala Met Ala Trp Glu Gly Glu Pro Met Arg His  
 305                      310                      315                      320  
 Asn Leu Gly Gly Asn Leu Gly Asp Pro Arg Ala Arg Ala Val Ser Val  
 325                      330                      335  
 Pro Leu Gly Gly Arg Val Ala Arg Phe Leu Gln Cys Arg Phe Leu Phe  
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 Ala Gly Pro Trp Leu Leu Phe Ser Glu Ile Ser Phe Ile Ser Asp Val  
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 Val Asn Asn Ser Ser Pro Ala Leu Gly Gly Thr Phe Pro Pro Ala Pro  
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 Trp Trp Pro Pro Gly Pro Pro Pro Thr Asn Phe Ser Ser Leu Glu Leu  
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 Glu Pro Arg Gly Gln Gln Pro Val Ala Lys Ala Glu Gly Ser Pro Thr  
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 420                      425                      430  
 Ile Ile Ala Leu Met Leu Trp Arg Leu His Trp Arg Arg Leu Leu Ser  
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 Lys Ala Glu Arg Arg Val Leu Glu Glu Glu Leu Thr Val His Leu Ser  
 450                      455                      460  
 Val Pro Gly Asp Thr Ile Leu Ile Asn Asn Arg Pro Gly Pro Arg Glu  
 465                      470                      475                      480  
 Pro Pro Pro Tyr Gln Glu Pro Arg Pro Arg Gly Asn Pro Pro His Ser  
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 Ala Pro Cys Val Pro Asn Gly Ser Ala Leu Leu Leu Ser Asn Pro Ala  
 500                      505                      510  
 Tyr Arg Leu Leu Leu Ala Thr Tyr Ala Arg Pro Pro Arg Gly Pro Gly  
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 Pro Pro Thr Pro Ala Trp Ala Lys Pro Thr Asn Thr Gln Ala Tyr Ser  
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 Gly Asp Tyr Met Glu Pro Glu Lys Pro Gly Ala Pro Leu Leu Pro Pro  
 545                      550                      555                      560

Pro Pro Gln Asn Ser Val Pro His Tyr Ala Glu Ala Asp Ile Val Thr  
565 570 575

Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ala Val Pro Ala Leu Pro  
580 585 590

Pro Gly Ala Val Gly Asp Gly Pro Pro Arg Val Asp Phe Pro Arg Ser  
595 600 605

Arg Leu Arg Phe Lys Glu Lys Leu Gly Glu Gly Gln Phe Gly Glu Val  
610 615 620

His Leu Cys Glu Val Asp Ser Pro Gln Asp Leu Val Ser Leu Asp Phe  
625 630 635 640

Pro Leu Asn Val Arg Lys Gly His Pro Leu Leu Val Ala Val Lys Ile  
645 650 655

Leu Arg Pro Asp Ala Thr Lys Asn Ala Ser Phe Ser Leu Phe Ser Arg  
660 665 670

Asn Asp Phe Leu Lys Glu Val Lys Ile Met Ser Arg Leu Lys Asp Pro  
675 680 685

Asn Ile Ile Arg Leu Leu Gly Val Cys Val Gln Asp Asp Pro Leu Cys  
690 695 700

Met Ile Thr Asp Tyr Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser  
705 710 715 720

Ala His Gln Leu Glu Asp Lys Ala Ala Glu Gly Ala Pro Gly Asp Gly  
725 730 735

Gln Ala Ala Gln Gly Pro Thr Ile Ser Tyr Pro Met Leu Leu His Val  
740 745 750

Ala Ala Gln Ile Ala Ser Gly Met Arg Tyr Leu Ala Thr Leu Asn Phe  
755 760 765

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Phe  
770 775 780

Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr Ala Gly  
785 790 795 800

Asp Tyr Tyr Arg Val Gln Gly Arg Ala Val Leu Pro Ile Arg Trp Met  
805 810 815

Ala Trp Glu Cys Ile Leu Met Gly Lys Phe Thr Thr Ala Ser Asp Val  
820 825 830

Trp Ala Phe Gly Val Thr Leu Trp Glu Val Leu Met Leu Cys Arg Ala  
835 840 845

Gln Pro Phe Gly Ser Ala His Arg Arg Ala Gly His Arg Glu Arg Gly  
850 855 860

Gly Val Leu Pro Gly Pro Gly Pro Ala Val Tyr Leu Ser Arg Pro Pro  
865 870 875 880

Ala Cys Pro Gln Gly Leu Tyr Glu Leu Met Leu Arg Cys Trp Ser Arg  
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gtcacc atg gaa gtg tca cca ttg cag cct gta aat gaa aat atg caa 168  
Met Glu Val Ser Pro Leu Gln Pro Val Asn Glu Asn Met Gln  
1 5 10

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Val Asn Lys Ile Lys Lys Asn Glu Asp Ala Lys Lys Arg Leu Ser Val  
15 20 25 30

gaa aga atc tat caa aag aaa aca caa ttg gaa cat att ttg ctc cgc 264  
Glu Arg Ile Tyr Gln Lys Lys Thr Gln Leu Glu His Ile Leu Leu Arg  
35 40 45

cca gac acc tac att ggt tct gtg gaa tta gtg acc cag caa atg tgg 312  
Pro Asp Thr Tyr Ile Gly Ser Val Glu Leu Val Thr Gln Gln Met Trp  
50 55 60

gtt tac gat gaa gat gtt ggc att aac tat agg gaa gtc act ttt gtt 360



Val	Tyr	Asp	Glu	Asp	Val	Gly	Ile	Asn	Tyr	Arg	Glu	Val	Thr	Phe	Val	
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Pro	Gly	Leu	Tyr	Lys	Ile	Phe	Asp	Glu	Ile	Leu	Val	Asn	Ala	Ala	Asp	
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aac	aaa	caa	agg	gac	cca	aaa	atg	tct	tgt	att	aga	gtc	aca	att	gat	456
Asn	Lys	Gln	Arg	Asp	Pro	Lys	Met	Ser	Cys	Ile	Arg	Val	Thr	Ile	Asp	
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Pro	Glu	Asn	Asn	Leu	Ile	Ser	Ile	Trp	Asn	Asn	Gly	Lys	Gly	Ile	Pro	
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Val	Val	Glu	His	Lys	Val	Glu	Lys	Met	Tyr	Val	Pro	Ala	Leu	Ile	Phe	
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Gly	Gln	Leu	Leu	Thr	Ser	Ser	Asn	Tyr	Asp	Asp	Asp	Glu	Lys	Lys	Val	
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Thr	Gly	Gly	Arg	Asn	Gly	Tyr	Gly	Ala	Lys	Leu	Cys	Asn	Ile	Phe	Ser	
	160					165					170					
acc	aaa	ttt	act	gtg	gaa	aca	gcc	agt	aga	gaa	tac	aag	aaa	atg	ttc	696
Thr	Lys	Phe	Thr	Val	Glu	Thr	Ala	Ser	Arg	Glu	Tyr	Lys	Lys	Met	Phe	
	175				180					185					190	
aaa	cag	aca	tgg	atg	gat	aat	atg	gga	aga	gct	ggt	gag	atg	gaa	ctc	744
Lys	Gln	Thr	Trp	Met	Asp	Asn	Met	Gly	Arg	Ala	Gly	Glu	Met	Glu	Leu	
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Lys	Pro	Phe	Asn	Gly	Glu	Asp	Tyr	Thr	Cys	Ile	Thr	Phe	Gln	Pro	Asp	
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Leu	Ser	Lys	Phe	Lys	Met	Gln	Ser	Leu	Asp	Lys	Asp	Ile	Val	Ala	Leu	
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Val	Phe	Leu	Asn	Gly	Asn	Lys	Leu	Pro	Val	Lys	Gly	Phe	Arg	Ser	Tyr	
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Val	Asp	Met	Tyr	Leu	Lys	Asp	Lys	Leu	Asp	Glu	Thr	Gly	Asn	Ser	Leu	
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aaa	gta	ata	cat	gaa	caa	gta	aac	cac	agg	tgg	gaa	gtg	tgt	tta	act	1032
Lys	Val	Ile	His	Glu	Gln	Val	Asn	His	Arg	Trp	Glu	Val	Cys	Leu	Thr	
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Thr	Ser	Lys	Gly	Gly	Arg	His	Val	Asp	Tyr	Val	Ala	Asp	Gln	Ile	Val	
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agc ctt cct gaa ttt gaa gag tgg aag agt tct act cca aat cat aaa	1944

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Gly	Gln	Thr	Thr	Thr	Tyr	Leu	Thr	Tyr	Asn	Asp	Phe	Ile	Asn	Lys	Glu	
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Leu	Ile	Leu	Phe	Ser	Asn	Ser	Asp	Asn	Glu	Arg	Ser	Ile	Pro	Ser	Met	
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Val	Ala	Glu	Met	Ser	Ser	Tyr	His	His	Gly	Glu	Met	Ser	Leu	Met	Met	
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Thr	Ile	Ile	Asn	Leu	Ala	Gln	Asn	Phe	Val	Gly	Ser	Asn	Asn	Leu	Asn	
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Asp Glu Asp Val Gly Ile Asn Tyr Arg Glu Val Thr Phe Val Pro Gly  
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Leu Tyr Lys Ile Phe Asp Glu Ile Leu Val Asn Ala Ala Asp Asn Lys  
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Gln Arg Asp Pro Lys Met Ser Cys Ile Arg Val Thr Ile Asp Pro Glu  
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Trp Pro Ser Leu Leu Arg His Arg Phe Leu Glu Glu Phe Ile Thr Pro  
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1160 1165 1170

Phe Ile Glu Glu Leu Glu Ala Val Glu Ala Lys Glu Lys Gln Asp  
1175 1180 1185

Glu Gln Val Gly Leu Pro Gly Lys Gly Gly Lys Ala Lys Gly Lys  
1190 1195 1200

Lys Thr Gln Met Ala Glu Val Leu Pro Ser Pro Arg Gly Gln Arg  
1205 1210 1215

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Val Ile Pro Arg Ile Thr Ile Glu Met Lys Ala Glu Ala Glu Lys
    1220                      1225          1230
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Lys Asn Lys Lys Lys Ile Lys Asn Glu Asn Thr Glu Gly Ser Pro

1235	1240	1245
Gln Glu Asp Gly Val Glu Leu Glu Gly Leu Lys Gln Arg Leu Glu 1250 1255 1260		
Lys Lys Gln Lys Arg Glu Pro Gly Thr Lys Thr Lys Lys Gln Thr 1265 1270 1275		
Thr Leu Ala Phe Lys Pro Ile Lys Lys Gly Lys Lys Arg Asn Pro 1280 1285 1290		
Trp Ser Asp Ser Glu Ser Asp Arg Ser Ser Asp Glu Ser Asn Phe 1295 1300 1305		
Asp Val Pro Pro Arg Glu Thr Glu Pro Arg Arg Ala Ala Thr Lys 1310 1315 1320		
Thr Lys Phe Thr Met Asp Leu Asp Ser Asp Glu Asp Phe Ser Asp 1325 1330 1335		
Phe Asp Glu Lys Thr Asp Asp Glu Asp Phe Val Pro Ser Asp Ala 1340 1345 1350		
Ser Pro Pro Lys Thr Lys Thr Ser Pro Lys Leu Ser Asn Lys Glu 1355 1360 1365		
Leu Lys Pro Gln Lys Ser Val Val Ser Asp Leu Glu Ala Asp Asp 1370 1375 1380		
Val Lys Gly Ser Val Pro Leu Ser Ser Ser Pro Pro Ala Thr His 1385 1390 1395		
Phe Pro Asp Glu Thr Glu Ile Thr Asn Pro Val Pro Lys Lys Asn 1400 1405 1410		
Val Thr Val Lys Lys Thr Ala Ala Lys Ser Gln Ser Ser Thr Ser 1415 1420 1425		
Thr Thr Gly Ala Lys Lys Arg Ala Ala Pro Lys Gly Thr Lys Arg 1430 1435 1440		
Asp Pro Ala Leu Asn Ser Gly Val Ser Gln Lys Pro Asp Pro Ala 1445 1450 1455		
Lys Thr Lys Asn Arg Arg Lys Arg Lys Pro Ser Thr Ser Asp Asp 1460 1465 1470		
Ser Asp Ser Asn Phe Glu Lys Ile Val Ser Lys Ala Val Thr Ser 1475 1480 1485		

Lys Lys Ser Lys Gly Glu Ser Asp Asp Phe His Met Asp Phe Asp  
1490 1495 1500

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Ile Lys Tyr Leu Glu Glu Ser Asp Glu Asp Asp Leu Phe  
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<212> DNA

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gggacccggg cgccccgcc tgcgcagcgc ccgccccgcg ccgcccccg cccgccctct      180
gtatctggcc cctgggcagc tgcccgggga ggcggccagc gagctggggc cgcgca atg      239
                                         Met
                                         1

tcg cac gga gcc ggg ctc gtc cgc acc acg tgc agc agc ggc agc gcg      287
Ser His Gly Ala Gly Leu Val Arg Thr Thr Cys Ser Ser Gly Ser Ala
          5                      10                      15

ctc gga ccc ggg gcc ggc gcg gcc cag ccc agc gcg agc ccc ttg gag      335
Leu Gly Pro Gly Ala Gly Ala Gln Pro Ser Ala Ser Pro Leu Glu
          20                      25                      30

ggg ctg ctg gac ctc agc tac ccc cgc acc cac gcg gcc ctg ctg aaa      383
Gly Leu Leu Asp Leu Ser Tyr Pro Arg Thr His Ala Ala Leu Leu Lys
          35                      40                      45

gtg gcg caa atg gtc acc ctg ctg att gcc ttc atc tgt gtg cgg agc      431
Val Ala Gln Met Val Thr Leu Leu Ile Ala Phe Ile Cys Val Arg Ser
          50                      55                      60                      65

tcc ctg tgg acc aac tac agc gcc tac agc tac ttt gaa gtg gtc acc      479
Ser Leu Trp Thr Asn Tyr Ser Ala Tyr Ser Tyr Phe Glu Val Val Thr
          70                      75                      80

att tgc gac ttg ata atg atc ctc gcc ttt tac ctg gtc cac ctc ttc      527
Ile Cys Asp Leu Ile Met Ile Leu Ala Phe Tyr Leu Val His Leu Phe
          85                      90                      95

cgc ttc tac cgc gtg ctc acc tgt atc agc tgg ccc ctg tcg gaa ctt      575

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 Leu His Tyr Leu Ile Gly Thr Leu Leu Leu Leu Ile Ala Ser Ile Val  
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gca gct tcc aag agt tac aac cag agc gga ctg gta gcc gga gcg atc 671  
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 130 135 140 145

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 Tyr Lys Ile Ser Cys Val Thr Gln Ser Thr Asp Ala Ala Val  
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gccggaaact cttcctccag ccttcggggg agaacatccc tcccattctg ggaaaggaaa 1001

gcagcctcca gggaaatggt ttctgccttc ctgcttctag aaccacctca ggtactgatg 1061

aaccccaact agcacagctg aagggtttg tgaatactcc cgcctaaatc ccttctactt 1121

cactcctcag gggagtgaag tgccttaaga aacaaagccc tgtcctaatt tatctagctt 1181

gtcagtcagg tcttagagat accctctttc ctgaagttag gcgtgcctgt agaaacacta 1241

tgtggtcagc ctgtccocaa ggagatcttg tgtctcctct ccatctctgc ctttggtacc 1301

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aaaaaaaaa 1369

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&lt;212&gt; PRT

&lt;213&gt; NM\_138410 chemokine-like factor super family 7, CKLFSF7

&lt;400&gt; 32

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Ala Leu Gly Pro Gly Ala Gly Ala Ala Gln Pro Ser Ala Ser Pro Leu  
 20 25 30

Glu Gly Leu Leu Asp Leu Ser Tyr Pro Arg Thr His Ala Ala Leu Leu  
 35 40 45

Lys Val Ala Gln Met Val Thr Leu Leu Ile Ala Phe Ile Cys Val Arg  
 50 55 60

Ser Ser Leu Trp Thr Asn Tyr Ser Ala Tyr Ser Tyr Phe Glu Val Val  
65 70 75 80

Thr Ile Cys Asp Leu Ile Met Ile Leu Ala Phe Tyr Leu Val His Leu  
85 90 95

Phe Arg Phe Tyr Arg Val Leu Thr Cys Ile Ser Trp Pro Leu Ser Glu  
100 105 110

Leu Leu His Tyr Leu Ile Gly Thr Leu Leu Leu Leu Ile Ala Ser Ile  
115 120 125

Val Ala Ala Ser Lys Ser Tyr Asn Gln Ser Gly Leu Val Ala Gly Ala  
130 135 140

Ile Phe Gly Phe Met Ala Thr Phe Leu Cys Met Ala Ser Ile Trp Leu  
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Ser Tyr Lys Ile Ser Cys Val Thr Gln Ser Thr Asp Ala Ala Val  
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<212> DNA

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<222> (458)..(2698)

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aggcctgata gactgattaa accacagaag gtgacctgct gagaaaagtg gtacaaatac 420  
tgggaaaaac ctgctcttct gcgttaagtg ggagaca atg tca caa gtt aaa agc 475  
Met Ser Gln Val Lys Ser  
1 5

tct tat toc tat gat gcc ccc tcg gat ttc atc aat ttt tca tcc ttg Ser Tyr Ser Tyr Asp Ala Pro Ser Asp Phe Ile Asn Phe Ser Ser Leu 10 15 20	523
gat gat gaa gga gat act caa aac ata gat tca tgg ttt gag gag aag Asp Asp Glu Gly Asp Thr Gln Asn Ile Asp Ser Trp Phe Glu Glu Lys 25 30 35	571
gcc aat ttg gag aat aag tta ctg ggg aag aat gga act gga ggg ctt Ala Asn Leu Glu Asn Lys Leu Leu Gly Lys Asn Gly Thr Gly Gly Leu 40 45 50	619
ttt cag ggc aaa act cct ttg aga aag gct aat ctt cag caa gct att Phe Gln Gly Lys Thr Pro Leu Arg Lys Ala Asn Leu Gln Gln Ala Ile 55 60 65 70	667
gtc aca cct ttg aaa cca gtt gac aac act tac tac aaa gag gca gaa Val Thr Pro Leu Lys Pro Val Asp Asn Thr Tyr Tyr Lys Glu Ala Glu 75 80 85	715
aaa gaa aat ctt gtg gaa caa tcc att ccg tca aat gct tgt tct tcc Lys Glu Asn Leu Val Glu Gln Ser Ile Pro Ser Asn Ala Cys Ser Ser 90 95 100	763
ctg gaa gtt gag gca gcc ata tca aga aaa act cca gcc cag cct cag Leu Glu Val Glu Ala Ala Ile Ser Arg Lys Thr Pro Ala Gln Pro Gln 105 110 115	811
aga aga tct ctt agg ctt tct gct cag aag gat ttg gaa cag aaa gaa Arg Arg Ser Leu Arg Leu Ser Ala Gln Lys Asp Leu Glu Gln Lys Glu 120 125 130	859
aag cat cat gta aaa atg aaa gcc aag aga tgt gcc act cct gta atc Lys His His Val Lys Met Lys Ala Lys Arg Cys Ala Thr Pro Val Ile 135 140 145 150	907
atc gat gaa att cta ccc tct aag aaa atg aaa gtt tct aac aac aaa Ile Asp Glu Ile Leu Pro Ser Lys Lys Met Lys Val Ser Asn Asn Lys 155 160 165	955
aag aag cca gag gaa gaa ggc agt gct cat caa gat act gct gaa aag Lys Lys Pro Glu Glu Glu Gly Ser Ala His Gln Asp Thr Ala Glu Lys 170 175 180	1003
aat gca tct tcc cca gag aaa gcc aag ggt aga cat act gtg cct tgt Asn Ala Ser Ser Pro Glu Lys Ala Lys Gly Arg His Thr Val Pro Cys 185 190 195	1051
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ctg gag aag agt atg aaa atg cag caa gag gtg gtg gag atg cgg aaa Leu Glu Lys Ser Met Lys Met Gln Gln Glu Val Val Glu Met Arg Lys 215 220 225 230	1147
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gtg aag aaa tca gtg agc cag gtc acc aaa tca gtt gac ttc cac ttc Val Lys Lys Ser Val Ser Gln Val Thr Lys Ser Val Asp Phe His Phe 250 255 260	1243
cgc aca gat gag cga atc aaa caa cat cct aag aac cag gag gaa tat Arg Thr Asp Glu Arg Ile Lys Gln His Pro Lys Asn Gln Glu Glu Tyr 265 270 275	1291



aag gaa gtg aac ttt aca tct gaa cta cga aag cat cct tca tct cct Lys Glu Val Asn Phe Thr Ser Glu Leu Arg Lys His Pro Ser Ser Pro 280 285 290	1339
gcc cga gtg act aag gga tgt acc att gtt aag cct ttc aac ctg tcc Ala Arg Val Thr Lys Gly Cys Thr Ile Val Lys Pro Phe Asn Leu Ser 295 300 305 310	1387
caa gga aag aaa aga aca ttt gat gaa aca gtt tct aca tat gtg ccc Gln Gly Lys Lys Arg Thr Phe Asp Glu Thr Val Ser Thr Tyr Val Pro 315 320 325	1435
ctt gca cag caa gtt gaa gac ttc cat aaa cga acc cct aac aga tat Leu Ala Gln Gln Val Glu Asp Phe His Lys Arg Thr Pro Asn Arg Tyr 330 335 340	1483
cat ttg agg agc aag aag gat gat att aac ctg tta ccc tcc aaa tct His Leu Arg Ser Lys Lys Asp Asp Ile Asn Leu Leu Pro Ser Lys Ser 345 350 355	1531
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gct gag gag ctc gag aaa ttg caa caa tac aaa ttc aaa gca cgt gaa Ala Glu Glu Leu Glu Lys Leu Gln Gln Tyr Lys Phe Lys Ala Arg Glu 395 400 405	1675
ctt gat ccc aga ata ctt gaa ggt ggg ccc atc ttg ccc aag aaa cca Leu Asp Pro Arg Ile Leu Glu Gly Gly Pro Ile Leu Pro Lys Lys Pro 410 415 420	1723
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cca gcc ttt gca ttg aag aac aga att cga atg ccc acc aaa gaa gat Pro Ala Phe Ala Leu Lys Asn Arg Ile Arg Met Pro Thr Lys Glu Asp 490 495 500	1963
gag gaa gag gac gaa ccg gta gtg ata aaa gct caa cct gtg cca cat Glu Glu Glu Asp Glu Pro Val Val Ile Lys Ala Gln Pro Val Pro His 505 510 515	2011
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ata tgc cct ttc tcg ttt gat tct cga gac aaa gaa cgt cag tta cag Ile Cys Pro Phe Ser Phe Asp Ser Arg Asp Lys Glu Arg Gln Leu Gln 535 540 545 550	2107

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gct gag gta gaa gcc cag aaa gcc cag cag ttg gag gag gcc aga cta Ala Glu Val Glu Ala Gln Lys Ala Gln Gln Leu Glu Glu Ala Arg Leu 680 685 690	2539
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Asn Gly Thr Gly Gly Leu Phe Gln Gly Lys Thr Pro Leu Arg Lys Ala  
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Asn Leu Gln Gln Ala Ile Val Thr Pro Leu Lys Pro Val Asp Asn Thr  
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Tyr Tyr Lys Glu Ala Glu Lys Glu Asn Leu Val Glu Gln Ser Ile Pro  
85 90 95

Ser Asn Ala Cys Ser Ser Leu Glu Val Glu Ala Ala Ile Ser Arg Lys  
100 105 110

Thr Pro Ala Gln Pro Gln Arg Arg Ser Leu Arg Leu Ser Ala Gln Lys  
115 120 125

Asp Leu Glu Gln Lys Glu Lys His His Val Lys Met Lys Ala Lys Arg  
130 135 140

Cys Ala Thr Pro Val Ile Ile Asp Glu Ile Leu Pro Ser Lys Lys Met  
145 150 155 160

Lys Val Ser Asn Asn Lys Lys Lys Pro Glu Glu Glu Gly Ser Ala His  
165 170 175

Gln Asp Thr Ala Glu Lys Asn Ala Ser Ser Pro Glu Lys Ala Lys Gly  
180 185 190

Arg His Thr Val Pro Cys Met Pro Pro Ala Lys Gln Lys Phe Leu Lys  
195 200 205

Ser Thr Glu Glu Gln Glu Leu Glu Lys Ser Met Lys Met Gln Gln Glu  
210 215 220

Val Val Glu Met Arg Lys Lys Asn Glu Glu Phe Lys Lys Leu Ala Leu  
225 230 235 240

Ala Gly Ile Gly Gln Pro Val Lys Lys Ser Val Ser Gln Val Thr Lys  
245 250 255

Ser Val Asp Phe His Phe Arg Thr Asp Glu Arg Ile Lys Gln His Pro  
260 265 270

Lys Asn Gln Glu Glu Tyr Lys Glu Val Asn Phe Thr Ser Glu Leu Arg  
275 280 285

Lys His Pro Ser Ser Pro Ala Arg Val Thr Lys Gly Cys Thr Ile Val  
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Lys Pro Phe Asn Leu Ser Gln Gly Lys Lys Arg Thr Phe Asp Glu Thr  
305 310 315 320

Val Ser Thr Tyr Val Pro Leu Ala Gln Gln Val Glu Asp Phe His Lys  
325 330 335

Arg Thr Pro Asn Arg Tyr His Leu Arg Ser Lys Lys Asp Asp Ile Asn  
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Leu Leu Pro Ser Lys Ser Ser Val Thr Lys Ile Cys Arg Asp Pro Gln  
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Thr Pro Val Leu Gln Thr Lys His Arg Ala Arg Ala Val Thr Cys Lys  
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Ser Thr Ala Glu Leu Glu Ala Glu Glu Leu Glu Lys Leu Gln Gln Tyr  
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Lys Phe Lys Ala Arg Glu Leu Asp Pro Arg Ile Leu Glu Gly Gly Pro  
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Ile Leu Pro Lys Lys Pro Pro Val Lys Pro Pro Thr Glu Pro Ile Gly  
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Phe Asp Leu Glu Ile Glu Lys Arg Ile Gln Glu Arg Glu Ser Lys Lys  
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Lys Thr Glu Asp Glu His Phe Glu Phe His Ser Arg Pro Cys Pro Thr  
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Ile Thr Val Pro Lys Ser Pro Ala Phe Ala Leu Lys Asn Arg Ile Arg  
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Met Pro Thr Lys Glu Asp Glu Glu Glu Asp Glu Pro Val Val Ile Lys  
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Ala Gln Pro Val Pro His Tyr Gly Val Pro Phe Lys Pro Gln Ile Pro  
 515 520 525

Glu Ala Arg Thr Val Glu Ile Cys Pro Phe Ser Phe Asp Ser Arg Asp  
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Lys Glu Arg Gln Leu Gln Lys Glu Lys Lys Ile Lys Glu Leu Gln Lys  
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Gly Glu Val Pro Lys Phe Lys Ala Leu Pro Leu Pro His Phe Asp Thr  
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Ile Asn Leu Pro Glu Lys Lys Val Lys Asn Val Thr Gln Ile Glu Pro  
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Phe Cys Leu Glu Thr Asp Arg Arg Gly Ala Leu Lys Ala Gln Thr Trp  
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Lys His Gln Leu Glu Glu Glu Leu Arg Gln Gln Lys Glu Ala Ala Cys  
 610 615 620

Phe Lys Ala Arg Pro Asn Thr Val Ile Ser Gln Glu Pro Phe Val Pro  
 625 630 635 640

Lys Lys Glu Lys Lys Ser Val Ala Glu Gly Leu Ser Gly Ser Leu Val  
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Gln Glu Pro Phe Gln Leu Ala Thr Glu Lys Arg Ala Lys Glu Arg Gln  
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Glu Leu Glu Lys Arg Met Ala Glu Val Glu Ala Gln Lys Ala Gln Gln  
 675 680 685

Leu Glu Glu Ala Arg Leu Gln Glu Glu Glu Gln Lys Lys Glu Glu Leu  
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Ala Arg Leu Arg Arg Glu Leu Val His Lys Ala Asn Pro Ile Arg Lys  
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 5 10 15

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 Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu Trp  
 20 25 30

ctc cga ttc gac tct cag acc aag agc atc ttc gag caa gaa act aat 261  
 Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu Thr Asn  
 35 40 45 50

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 Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly Ala  
 55 60 65

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 70 75 80

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 Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu Leu Val  
 85 90 95

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 Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser His Lys  
 100 105 110

gat gag gtg att aag gaa gtc cag gag ttt tac aag gac acc tac aac 501  
 Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr Asn  
 115 120 125 130

aag ctg aaa acc aag gat gag ccc cag cgg gaa acg ctg aaa gcc atc 549

Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala Ile  
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 His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln Phe  
 150 155 160  
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 Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr Val  
 165 170 175  
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Gly Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly  
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Ala Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu  
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Leu Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser  
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 Leu Thr Ser Gly Pro Gln His Arg Lys Ala Ala Trp Ser Gly Gly Val  
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Ser	Trp	His	Thr	Thr	Lys	Ser	Gly	Glu	Lys	Gln	Pro	Asp	Ala	Ser	Met	
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Pro	Ala	Arg	Ser	Asp	Ser	Tyr	Ala	Ala	Phe	Arg	His	Arg	Glu	Arg	Pro	
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Thr	Val	Leu	Glu	Lys	Ser	Pro	Glu	Asn	Ser	Pro	Pro	Val	Lys	Pro	Lys	
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Ser	Ile	Tyr	Ala	Val	Pro	Ser	Leu	Glu	Pro	His	Phe	Ala	Gln	Val	Pro	
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Gln	Pro	Ser	Val	Ser	Ser	Asn	Gly	Met	Leu	Tyr	Pro	Ala	Leu	Ala	Lys	
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Phe	Cys	Gln	Pro	Leu	Glu	His	Asp	Leu	Leu	Ser	Pro	Val	Glu	Lys	Lys	
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Val	Pro	Glu	Asn	Glu	Glu	Asp	Ala	Ser	Leu	Lys	Arg	His	Leu	Thr	Pro	
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Ala	Trp	Gln	Ala	Gly	Glu	Asp	Lys	Arg	Ser	Ser	Arg	Leu	Ser	Glu	Pro	
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Tyr	Pro	Arg	Pro	Glu	Gly	Arg	Thr	Gly	Ala	Ser	Ala	Ser	Phe	Asn	Ser	
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Phe	Ser	Glu	Ser	Ala	Glu	Pro	Leu	Gly	Asn	Gly	Glu	Gln	His	Phe	Lys	
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Pro	Leu	Leu	Asp	Ala	Pro	Phe	Ser	Arg	Ala	Tyr	Arg	Asn	Ser	Ile	Lys	
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Asp	Ala	Gln	Ser	Arg	Val	Leu	Gly	Ala	Thr	Ser	Phe	Arg	Arg	Arg	Asp	
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Leu	Glu	Leu	Gly	Ala	Pro	Val	Ala	Ser	Arg	Ser	Trp	Arg	Pro	Arg	Pro	
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Ser Ser Ala His Val Gly Leu Arg Ser Pro Glu Ala Ser Ala Ser Ala	965	970	975	
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gac ctg gcc agg ccc gtg ccc cct gcc gcc cgg aga ggt gct cgc cgg				3981
Asp Leu Ala Arg Pro Val Pro Pro Ala Ala Arg Arg Gly Ala Arg Arg	995	1000	1005	
cgc ctg act ccc gag cag aag aag cgc tcc tac tcg gag ccc gag				4026
Arg Leu Thr Pro Glu Gln Lys Lys Arg Ser Tyr Ser Glu Pro Glu	1010	1015	1020	
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Lys Met Asn Glu Val Gly Ile Val Glu Glu Ala Glu Pro Ala Pro	1025	1030	1035	
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Leu Gly Pro Gln Arg Asn Gly Met Arg Phe Pro Glu Ser Ser Val	1040	1045	1050	
gcc gac cgg cgc cgt ctc ttc gag cgc gat gcc aag gcc tgc tcc				4161
Ala Asp Arg Arg Arg Leu Phe Glu Arg Asp Gly Lys Ala Cys Ser	1055	1060	1065	
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Thr Leu Ser Leu Ser Gly Pro Glu Leu Lys Gln Phe Gln Gln Ser	1070	1075	1080	
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Ala Leu Ala Asp Tyr Ile Gln Arg Lys Thr Gly Lys Arg Pro Thr	1085	1090	1095	
tcc gcc gcc ggc tgc agc ctc cag gag ccc ggg cca ctg cgt gag				4296
Ser Ala Ala Gly Cys Ser Leu Gln Glu Pro Gly Pro Leu Arg Glu	1100	1105	1110	
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Arg Ala Gln Ser Ala Tyr Leu Gln Pro Gly Pro Ala Ala Leu Glu	1115	1120	1125	
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Gly Ser Gly Leu Ala Ser Ala Ser Ser Leu Ser Ser Leu Arg Glu	1130	1135	1140	
ccc agc ctg cag ccc cgc agg gag gcc acg ctc ctg ccg gcc aca				4431
Pro Ser Leu Gln Pro Arg Arg Glu Ala Thr Leu Leu Pro Ala Thr	1145	1150	1155	
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Val Ala Glu Thr Gln Gln Ala Pro Arg Asp Arg Ser Ser Ser Phe	1160	1165	1170	
gcc ggt gcc cgc cgc ctc ggg gaa cgg cga cgc ggg gac ctg ctt				4521
Ala Gly Gly Arg Arg Leu Gln Glu Arg Arg Arg Gly Asp Leu Leu	1175	1180	1185	
agc gga gca aac ggt gga aca agg ggc acc cag aga ggg gat gag				4566
Ser Gly Ala Asn Gly Gly Thr Arg Gly Thr Gln Arg Gly Asp Glu	1190	1195	1200	
acc ccc agg gag cca tcc tcc tgg ggg gcc agg gcc ggg aag tcc				4611
Thr Pro Arg Glu Pro Ser Ser Trp Gly Ala Arg Ala Gly Lys Ser	1205	1210	1215	
atg tcg gcc gag gac ctg ctg gaa cgc tcg gac gtc ctt gcg ggc				4656

Met	Ser	Ala	Glu	Asp	Leu	Leu	Glu	Arg	Ser	Asp	Val	Leu	Ala	Gly		
1220						1225					1230					
cct	gtc	cat	gtg	agg	tcc	agg	tca	tct	ccc	gcc	acc	gca	gac	aag	4701	
Pro	Val	His	Val	Arg	Ser	Arg	Ser	Ser	Pro	Ala	Thr	Ala	Asp	Lys		
1235						1240					1245					
cgc	cag	gat	gtg	ctt	ttg	ggg	caa	gac	agt	ggc	ttt	ggt	ctt	gtg	4746	
Arg	Gln	Asp	Val	Leu	Leu	Gly	Gln	Asp	Ser	Gly	Phe	Gly	Leu	Val		
1250						1255					1260					
aag	gat	cca	tgt	tat	ttg	gct	ggg	cct	gga	tct	agg	tca	ctc	agt	4791	
Lys	Asp	Pro	Cys	Tyr	Leu	Ala	Gly	Pro	Gly	Ser	Arg	Ser	Leu	Ser		
1265						1270					1275					
tgt	tca	gaa	aga	ggc	caa	gaa	gag	atg	ctg	ctg	ctc	ttc	cac	cat	4836	
Cys	Ser	Glu	Arg	Gly	Gln	Glu	Glu	Met	Leu	Leu	Leu	Phe	His	His		
1280						1285					1290					
ctc	acc	cct	cgt	tgg	ggg	ggg	tca	ggc	tgc	aaa	gcc	att	ggg	gat	4881	
Leu	Thr	Pro	Arg	Trp	Gly	Gly	Ser	Gly	Cys	Lys	Ala	Ile	Gly	Asp		
1295						1300					1305					
tcc	tcc	gtt	cct	agt	gaa	tgt	cct	gga	acc	ctg	gac	cat	cag	agg	4926	
Ser	Ser	Val	Pro	Ser	Glu	Cys	Pro	Gly	Thr	Leu	Asp	His	Gln	Arg		
1310						1315					1320					
caa	gcc	agt	agg	aca	ccc	tgc	ccc	agg	cca	cca	ctg	gca	gga	acg	4971	
Gln	Ala	Ser	Arg	Thr	Pro	Cys	Pro	Arg	Pro	Pro	Leu	Ala	Gly	Thr		
1325						1330					1335					
caa	ggg	ctg	gtc	aca	gac	acc	agg	gct	gca	ccc	ctg	acc	cca	att	5016	
Gln	Gly	Leu	Val	Thr	Asp	Thr	Arg	Ala	Ala	Pro	Leu	Thr	Pro	Ile		
1340						1345					1350					
ggc	acc	cct	ctg	cct	tca	gcc	att	ccc	tct	ggc	tac	tgc	tca	cag	5061	
Gly	Thr	Pro	Leu	Pro	Ser	Ala	Ile	Pro	Ser	Gly	Tyr	Cys	Ser	Gln		
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gac	ggg	cag	aca	ggg	cga	cag	cct	ctc	ccg	ccc	tac	acc	cct	gcc	5106	
Asp	Gly	Gln	Thr	Gly	Arg	Gln	Pro	Leu	Pro	Pro	Tyr	Thr	Pro	Ala		
1370						1375					1380					
atg	atg	cac	aga	agc	aat	ggg	cac	acc	ctg	acc	cag	cct	ccc	ggg	5151	
Met	Met	His	Arg	Ser	Asn	Gly	His	Thr	Leu	Thr	Gln	Pro	Pro	Gly		
1385						1390					1395					
cca	aga	ggc	tgt	gag	ggc	gat	ggc	cca	gag	cat	ggg	gta	gaa	gag	5196	
Pro	Arg	Gly	Cys	Glu	Gly	Asp	Gly	Pro	Glu	His	Gly	Val	Glu	Glu		
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Gly	Thr	Arg	Lys	Arg	Val	Ser	Leu	Pro	Gln	Trp	Pro	Pro	Pro	Ser		
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Arg	Ala	Lys	Trp	Ala	His	Ala	Ala	Arg	Glu	Asp	Ser	Leu	Pro	Glu		
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gaa	tcc	tca	gcc	cct	gat	ttt	gca	aac	ctg	aag	cac	tat	caa	aaa	5331	
Glu	Ser	Ser	Ala	Pro	Asp	Phe	Ala	Asn	Leu	Lys	His	Tyr	Gln	Lys		
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cag	cag	agt	ctt	cca	agt	tta	tgc	agc	act	tct	gac	cca	gac	aca	5376	
Gln	Gln	Ser	Leu	Pro	Ser	Leu	Cys	Ser	Thr	Ser	Asp	Pro	Asp	Thr		
1460						1465					1470					
cct	ctt	ggg	gcc	ccg	agc	act	cca	ggg	agg	atc	tcc	ctc	cga	ata	5421	

Pro Leu Gly Ala Pro Ser Thr	Pro Gly Arg Ile Ser	Leu Arg Ile	
1475	1480	1485	
tct gag tct gtc ctg cgg gac	tcc ccg cca cct cat	gag gat tat	5466
Ser Glu Ser Val Leu Arg Asp	Ser Pro Pro Pro His	Glu Asp Tyr	
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gaa gac gaa gtg ttt gtg agg	gat ccg cac ccc aag	gcc acg tcc	5511
Glu Asp Glu Val Phe Val Arg	Asp Pro His Pro Lys	Ala Thr Ser	
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agc ccc aca ttt gaa cct ctt	ccc cca ccc cca cct	cct cca ccg	5556
Ser Pro Thr Phe Glu Pro Leu	Pro Pro Pro Pro Pro	Pro Pro Pro	
1520	1525	1530	
agt cag gaa acc ccg gtg tat	agc atg gat gac ttc	cct cca cct	5601
Ser Gln Glu Thr Pro Val Tyr	Ser Met Asp Asp Phe	Pro Pro Pro	
1535	1540	1545	
cct ccc cac act gta tgt gag	gcg cag ctg gac agt	gag gat ccc	5646
Pro Pro His Thr Val Cys Glu	Ala Gln Leu Asp Ser	Glu Asp Pro	
1550	1555	1560	
gag ggg cca cgc ccc agc ttc	aac aaa ctt tct aaa	gtg aca att	5691
Glu Gly Pro Arg Pro Ser Phe	Asn Lys Leu Ser Lys	Val Thr Ile	
1565	1570	1575	
gca agg gaa agg cac atg cct	ggt gca gcc cat gtg	gta ggt agt	5736
Ala Arg Glu Arg His Met Pro	Gly Ala Ala His Val	Val Gly Ser	
1580	1585	1590	
cag aca ctg gct tcc aga ctc	caa act tct atc aag	ggt tca gag	5781
Gln Thr Leu Ala Ser Arg Leu	Gln Thr Ser Ile Lys	Gly Ser Glu	
1595	1600	1605	
gct gag tcc aca cca ccc tcc	ttc atg agc gtt cac	gcc caa ctt	5826
Ala Glu Ser Thr Pro Pro Ser	Phe Met Ser Val His	Ala Gln Leu	
1610	1615	1620	
gct ggg tct ctt ggt ggg cag	cca gca ccc atc cag	act caa agc	5871
Ala Gly Ser Leu Gly Gly Gln	Pro Ala Pro Ile Gln	Thr Gln Ser	
1625	1630	1635	
ctc agc cat gat cca gtc agt	gga act cag ggt tta	gaa aag aaa	5916
Leu Ser His Asp Pro Val Ser	Gly Thr Gln Gly Leu	Glu Lys Lys	
1640	1645	1650	
gtc agt cct gat cct cag aag	agt tca gaa gac atc	aga aca gag	5961
Val Ser Pro Asp Pro Gln Lys	Ser Ser Glu Asp Ile	Arg Thr Glu	
1655	1660	1665	
gct ttg gcc aag gaa att gtc	cac caa gac aaa tct	cta gca gac	6006
Ala Leu Ala Lys Glu Ile Val	His Gln Asp Lys Ser	Leu Ala Asp	
1670	1675	1680	
att ttg gat cca gac tcc agg	ctg aag aca aca atg	gac ctg atg	6051
Ile Leu Asp Pro Asp Ser Arg	Leu Lys Thr Thr Met	Asp Leu Met	
1685	1690	1695	
gaa ggt ttg ttt ccc cga gat	gtg aac ttg ctg aag	gaa aac agt	6096
Glu Gly Leu Phe Pro Arg Asp	Val Asn Leu Leu Lys	Glu Asn Ser	
1700	1705	1710	
gta aag agg aag gcc ata cag	aga act gtc agc tct	tca gga tgt	6141
Val Lys Arg Lys Ala Ile Gln	Arg Thr Val Ser Ser	Ser Gly Cys	
1715	1720	1725	
gaa ggc aag agg aat gaa gac	aag gaa gca gtg agc	atg ttg gtt	6186

Glu	Gly	Lys	Arg	Asn	Glu	Asp	Lys	Glu	Ala	Val	Ser	Met	Leu	Val	
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Asn	Cys	Pro	Ala	Tyr	Tyr	Ser	Val	Ser	Ala	Pro	Lys	Ala	Glu	Leu	
1745						1750					1755				
ctg	aac	aaa	atc	aaa	gag	atg	cca	gca	gaa	gtg	aat	gag	gaa	gag	6276
Leu	Asn	Lys	Ile	Lys	Glu	Met	Pro	Ala	Glu	Val	Asn	Glu	Glu	Glu	
1760						1765					1770				
gaa	cag	gca	gat	gtc	aat	gaa	aag	aag	gct	gag	ctc	att	gga	agt	6321
Glu	Gln	Ala	Asp	Val	Asn	Glu	Lys	Lys	Ala	Glu	Leu	Ile	Gly	Ser	
1775						1780					1785				
ctc	acc	cac	aag	ctg	gag	acc	ctc	cag	gag	gcg	aag	ggg	agc	ctg	6366
Leu	Thr	His	Lys	Leu	Glu	Thr	Leu	Gln	Glu	Ala	Lys	Gly	Ser	Leu	
1790						1795					1800				
ctc	acg	gac	atc	aag	ctc	aac	aac	gcc	ctg	gga	gaa	gag	gtg	gag	6411
Leu	Thr	Asp	Ile	Lys	Leu	Asn	Asn	Ala	Leu	Gly	Glu	Glu	Val	Glu	
1805						1810					1815				
gct	ctg	atc	agc	gag	ctc	tgc	aag	ccc	aat	gag	ttt	gac	aag	tat	6456
Ala	Leu	Ile	Ser	Glu	Leu	Cys	Lys	Pro	Asn	Glu	Phe	Asp	Lys	Tyr	
1820						1825					1830				
agg	atg	ttc	ata	ggg	gat	ttg	gac	aag	gtg	gtc	aac	ctg	ctg	ctc	6501
Arg	Met	Phe	Ile	Gly	Asp	Leu	Asp	Lys	Val	Val	Asn	Leu	Leu	Leu	
1835						1840					1845				
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Ser	Leu	Ser	Gly	Arg	Leu	Ala	Arg	Val	Glu	Asn	Val	Leu	Ser	Gly	
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Leu	Gly	Glu	Asp	Ala	Ser	Asn	Glu	Glu	Arg	Ser	Ser	Leu	Tyr	Glu	
1865						1870					1875				
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Lys	Arg	Lys	Ile	Leu	Ala	Gly	Gln	His	Glu	Asp	Ala	Arg	Glu	Leu	
1880						1885					1890				
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Lys	Glu	Asn	Leu	Asp	Arg	Arg	Glu	Arg	Val	Val	Leu	Gly	Ile	Leu	
1895						1900					1905				
gcc	aat	tac	ctt	tca	gag	gag	cag	ctc	cag	gac	tac	cag	cac	ttc	6726
Ala	Asn	Tyr	Leu	Ser	Glu	Glu	Gln	Leu	Gln	Asp	Tyr	Gln	His	Phe	
1910						1915					1920				
gtg	aaa	atg	aag	tcc	acg	ctc	ctc	att	gag	caa	cgg	aag	ctg	gat	6771
Val	Lys	Met	Lys	Ser	Thr	Leu	Leu	Ile	Glu	Gln	Arg	Lys	Leu	Asp	
1925						1930					1935				
gac	aag	atc	aag	ctg	ggc	cag	gag	cag	gtc	aag	tgt	ctg	ctg	gag	6816
Asp	Lys	Ile	Lys	Leu	Gly	Gln	Glu	Gln	Val	Lys	Cys	Leu	Leu	Glu	
1940						1945					1950				
agc	ctg	ccc	tca	gat	ttc	att	ccc	aag	gct	ggg	gcc	ctg	gct	ctg	6861
Ser	Leu	Pro	Ser	Asp	Phe	Ile	Pro	Lys	Ala	Gly	Ala	Leu	Ala	Leu	
1955						1960					1965				
ccc	cca	aac	ctc	acg	agt	gag	ccc	att	cct	gct	ggg	ggc	tgt	act	6906
Pro	Pro	Asn	Leu	Thr	Ser	Glu	Pro	Ile	Pro	Ala	Gly	Gly	Cys	Thr	
1970						1975					1980				
ttc	agt	ggt	att	ttc	cca	aca	tta	acc	tct	cca	ctt	taacctcttc			6952



Phe Ser Gly Ile Phe Pro Thr Leu Thr Ser Pro Leu  
1985 1990 1995

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aaatggaaaa gatcactatg ttgtgtgtgc taaccactta ttgtattctg tttgtgtgtg 7492  
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aagat 7557

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<212> PRT

<213> NM\_020859 ShrmL, Shroom-related protein

<400> 38

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Gly Gly Ala Pro Trp Gly Phe Thr Leu Lys Gly Gly Leu Glu His Gly  
35 40 45

Glu Pro Leu Ile Ile Ser Lys Val Glu Glu Gly Gly Lys Ala Asp Thr  
50 55 60

Leu Ser Ser Lys Leu Gln Ala Gly Asp Glu Val Val His Ile Asn Glu  
65 70 75 80

Val Thr Leu Ser Ser Ser Arg Lys Glu Ala Val Ser Leu Val Lys Gly  
85 90 95

Ser Tyr Lys Thr Leu Arg Leu Val Val Arg Arg Asp Val Cys Thr Asp  
100 105 110

Pro Gly His Ala Asp Thr Gly Ala Ser Asn Phe Val Ser Pro Glu His  
115 120 125

Leu Thr Ser Gly Pro Gln His Arg Lys Ala Ala Trp Ser Gly Gly Val  
130 135 140

Lys Leu Arg Leu Lys His Arg Ser Ser Glu Pro Ala Gly Arg Pro His  
145 150 155 160

Ser Trp His Thr Thr Lys Ser Gly Glu Lys Gln Pro Asp Ala Ser Met  
165 170 175

Met Gln Ile Ser Gln Gly Met Ile Gly Pro Pro Trp His Gln Ser Tyr  
180 185 190

His Ser Ser Ser Ser Thr Ser Asp Leu Ser Asn Tyr Asp His Ala Tyr  
195 200 205

Leu Arg Arg Ser Pro Asp Gln Cys Ser Ser Gln Gly Ser Met Glu Ser  
210 215 220

Leu Glu Pro Ser Gly Ala Tyr Pro Pro Cys His Leu Ser Pro Ala Lys  
225 230 235 240

Ser Thr Gly Ser Ile Asp Gln Leu Ser His Phe His Asn Lys Arg Asp  
245 250 255

Ser Ala Tyr Ser Ser Phe Ser Thr Ser Ser Ser Ile Leu Glu Tyr Pro  
260 265 270

His Pro Gly Ile Ser Ala Arg Glu Arg Ser Gly Ser Met Asp Asn Thr  
275 280 285

Ser Ala Arg Gly Gly Leu Leu Glu Gly Met Arg Gln Ala Asp Ile Arg  
290 295 300

Tyr Val Lys Thr Val Tyr Asp Thr Arg Arg Gly Val Ser Ala Glu Tyr  
305 310 315 320

Glu Val Asn Ser Ser Ala Leu Leu Leu Gln Gly Arg Glu Ala Arg Ala  
325 330 335

Ser Ala Asn Gly Gln Gly Tyr Asp Lys Trp Ser Asn Ile Pro Arg Gly  
340 345 350

Lys Gly Val Pro Pro Pro Ser Trp Ser Gln Gln Cys Pro Ser Ser Leu  
355 360 365

Glu Thr Ala Thr Asp Asn Leu Pro Pro Lys Val Gly Ala Pro Leu Pro  
370 375 380

Pro Ala Arg Ser Asp Ser Tyr Ala Ala Phe Arg His Arg Glu Arg Pro  
385 390 395 400

Ser Ser Trp Ser Ser Leu Asp Gln Lys Arg Leu Cys Arg Pro Gln Ala  
405 410 415

Asn Ser Leu Gly Ser Leu Lys Ser Pro Phe Ile Glu Glu Gln Leu His  
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Thr Val Leu Glu Lys Ser Pro Glu Asn Ser Pro Pro Val Lys Pro Lys  
435 440 445

His Asn Tyr Thr Gln Lys Ala Gln Pro Gly Gln Pro Leu Leu Pro Thr  
450 455 460

Ser Ile Tyr Ala Val Pro Ser Leu Glu Pro His Phe Ala Gln Val Pro  
465 470 475 480

Gln Pro Ser Val Ser Ser Asn Gly Met Leu Tyr Pro Ala Leu Ala Lys  
485 490 495

Glu Ser Gly Tyr Ile Ala Pro Gln Gly Ala Cys Asn Lys Met Ala Thr  
500 505 510

Ile Asp Glu Asn Gly Asn Gln Asn Gly Ser Gly Arg Pro Gly Phe Ala  
515 520 525

Phe Cys Gln Pro Leu Glu His Asp Leu Leu Ser Pro Val Glu Lys Lys  
530 535 540

Pro Glu Ala Thr Ala Lys Tyr Val Pro Ser Lys Val His Phe Cys Ser  
545 550 555 560

Val Pro Glu Asn Glu Glu Asp Ala Ser Leu Lys Arg His Leu Thr Pro  
565 570 575

Pro Gln Gly Asn Ser Pro His Ser Asn Glu Arg Lys Ser Thr His Ser  
580 585 590

Asn Lys Pro Ser Ser His Pro His Ser Leu Lys Cys Pro Gln Ala Gln  
595 600 605

Ala Trp Gln Ala Gly Glu Asp Lys Arg Ser Ser Arg Leu Ser Glu Pro  
610 615 620

Trp Glu Gly Asp Phe Gln Glu Asp His Asn Ala Asn Leu Trp Arg Arg  
625 630 635 640

Leu Glu Arg Glu Gly Leu Gly Gln Ser Leu Ser Gly Asn Phe Gly Lys  
645 650 655

Thr Lys Ser Ala Phe Ser Ser Leu Gln Asn Ile Pro Glu Ser Leu Arg  
660 665 670

Arg His Ser Ser Leu Glu Leu Gly Arg Gly Thr Gln Glu Gly Tyr Pro  
675 680 685

Gly Gly Arg Pro Thr Cys Ala Val Asn Thr Lys Ala Glu Asp Pro Gly  
690 695 700

Arg Lys Ala Ala Pro Asp Leu Gly Ser His Leu Asp Arg Gln Val Ser  
705 710 715 720

Tyr Pro Arg Pro Glu Gly Arg Thr Gly Ala Ser Ala Ser Phe Asn Ser  
725 730 735

Thr Asp Pro Ser Pro Glu Glu Pro Pro Ala Pro Ser His Pro His Thr  
740 745 750

Ser Ser Leu Gly Arg Arg Gly Pro Gly Pro Gly Ser Ala Ser Ala Leu  
755 760 765

Gln Gly Phe Gln Tyr Gly Lys Pro His Cys Ser Val Leu Glu Lys Val  
770 775 780

Ser Lys Phe Glu Gln Arg Glu Gln Gly Ser Gln Arg Pro Ser Val Gly  
785 790 795 800

Gly Ser Gly Phe Gly His Asn Tyr Arg Pro His Arg Thr Val Ser Thr  
805 810 815

Ser Ser Thr Ser Gly Asn Asp Phe Glu Glu Thr Lys Ala His Ile Arg  
820 825 830

Phe Ser Glu Ser Ala Glu Pro Leu Gly Asn Gly Glu Gln His Phe Lys  
835 840 845

Asn Gly Glu Leu Lys Leu Glu Glu Ala Ser Arg Gln Pro Cys Gly Gln  
850 855 860

Gln Leu Ser Gly Gly Ala Ser Asp Ser Gly Arg Gly Pro Gln Arg Pro  
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Asp Ala Arg Leu Leu Arg Ser Gln Ser Thr Phe Gln Leu Ser Ser Glu  
885 890 895

Pro Glu Arg Glu Pro Glu Trp Arg Asp Arg Pro Gly Ser Pro Glu Ser  
900 905 910

Pro Leu Leu Asp Ala Pro Phe Ser Arg Ala Tyr Arg Asn Ser Ile Lys  
915 920 925

Asp Ala Gln Ser Arg Val Leu Gly Ala Thr Ser Phe Arg Arg Arg Asp  
930 935 940

Leu Glu Leu Gly Ala Pro Val Ala Ser Arg Ser Trp Arg Pro Arg Pro  
 945 950 955 960

Ser Ser Ala His Val Gly Leu Arg Ser Pro Glu Ala Ser Ala Ser Ala  
 965 970 975

Ser Pro His Thr Pro Arg Glu Arg His Ser Val Thr Pro Ala Glu Gly  
 980 985 990

Asp Leu Ala Arg Pro Val Pro Pro Ala Ala Arg Arg Gly Ala Arg Arg  
 995 1000 1005

Arg Leu Thr Pro Glu Gln Lys Lys Arg Ser Tyr Ser Glu Pro Glu  
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Lys Met Asn Glu Val Gly Ile Val Glu Glu Ala Glu Pro Ala Pro  
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Leu Gly Pro Gln Arg Asn Gly Met Arg Phe Pro Glu Ser Ser Val  
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Ala Asp Arg Arg Arg Leu Phe Glu Arg Asp Gly Lys Ala Cys Ser  
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Thr Leu Ser Leu Ser Gly Pro Glu Leu Lys Gln Phe Gln Gln Ser  
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Ala Leu Ala Asp Tyr Ile Gln Arg Lys Thr Gly Lys Arg Pro Thr  
 1085 1090 1095

Ser Ala Ala Gly Cys Ser Leu Gln Glu Pro Gly Pro Leu Arg Glu  
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Arg Ala Gln Ser Ala Tyr Leu Gln Pro Gly Pro Ala Ala Leu Glu  
 1115 1120 1125

Gly Ser Gly Leu Ala Ser Ala Ser Ser Leu Ser Ser Leu Arg Glu  
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Pro Ser Leu Gln Pro Arg Arg Glu Ala Thr Leu Leu Pro Ala Thr  
 1145 1150 1155

Val Ala Glu Thr Gln Gln Ala Pro Arg Asp Arg Ser Ser Ser Phe  
 1160 1165 1170

Ala Gly Gly Arg Arg Leu Gly Glu Arg Arg Arg Gly Asp Leu Leu  
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Ser Gly Ala Asn Gly Gly Thr Arg Gly Thr Gln Arg Gly Asp Glu  
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Thr Pro Arg Glu Pro Ser Ser Trp Gly Ala Arg Ala Gly Lys Ser  
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 Pro Val His Val Arg Ser Arg Ser Ser Pro Ala Thr Ala Asp Lys  
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 Lys Asp Pro Cys Tyr Leu Ala Gly Pro Gly Ser Arg Ser Leu Ser  
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 Gly Thr Pro Leu Pro Ser Ala Ile Pro Ser Gly Tyr Cys Ser Gln  
 1355 1360 1365  
 Asp Gly Gln Thr Gly Arg Gln Pro Leu Pro Pro Tyr Thr Pro Ala  
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 Met Met His Arg Ser Asn Gly His Thr Leu Thr Gln Pro Pro Gly  
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 Pro Arg Gly Cys Glu Gly Asp Gly Pro Glu His Gly Val Glu Glu  
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 Glu Ser Ser Ala Pro Asp Phe Ala Asn Leu Lys His Tyr Gln Lys  
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Gln Gln Ser Leu Pro Ser Leu Cys Ser Thr Ser Asp Pro Asp Thr  
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 Pro Leu Gly Ala Pro Ser Thr Pro Gly Arg Ile Ser Leu Arg Ile  
 1475 1480 1485  
 Ser Glu Ser Val Leu Arg Asp Ser Pro Pro Pro His Glu Asp Tyr  
 1490 1495 1500  
 Glu Asp Glu Val Phe Val Arg Asp Pro His Pro Lys Ala Thr Ser  
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 Ser Pro Thr Phe Glu Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro  
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 Ser Gln Glu Thr Pro Val Tyr Ser Met Asp Asp Phe Pro Pro Pro  
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 Ala Arg Glu Arg His Met Pro Gly Ala Ala His Val Val Gly Ser  
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 1625 1630 1635  
 Leu Ser His Asp Pro Val Ser Gly Thr Gln Gly Leu Glu Lys Lys  
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 Val Ser Pro Asp Pro Gln Lys Ser Ser Glu Asp Ile Arg Thr Glu  
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 Ala Leu Ala Lys Glu Ile Val His Gln Asp Lys Ser Leu Ala Asp  
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 Ile Leu Asp Pro Asp Ser Arg Leu Lys Thr Thr Met Asp Leu Met  
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 Glu Gly Leu Phe Pro Arg Asp Val Asn Leu Leu Lys Glu Asn Ser  
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Val Lys Arg Lys Ala Ile Gln Arg Thr Val Ser Ser Ser Gly Cys  
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 Asn Cys Pro Ala Tyr Tyr Ser Val Ser Ala Pro Lys Ala Glu Leu  
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 Glu Gln Ala Asp Val Asn Glu Lys Lys Ala Glu Leu Ile Gly Ser  
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 Leu Thr His Lys Leu Glu Thr Leu Gln Glu Ala Lys Gly Ser Leu  
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 Ala Leu Ile Ser Glu Leu Cys Lys Pro Asn Glu Phe Asp Lys Tyr  
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 Arg Met Phe Ile Gly Asp Leu Asp Lys Val Val Asn Leu Leu Leu  
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 Ser Leu Ser Gly Arg Leu Ala Arg Val Glu Asn Val Leu Ser Gly  
 1850 1855 1860  
 Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu  
 1865 1870 1875  
 Lys Arg Lys Ile Leu Ala Gly Gln His Glu Asp Ala Arg Glu Leu  
 1880 1885 1890  
 Lys Glu Asn Leu Asp Arg Arg Glu Arg Val Val Leu Gly Ile Leu  
 1895 1900 1905  
 Ala Asn Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe  
 1910 1915 1920  
 Val Lys Met Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp  
 1925 1930 1935  
 Asp Lys Ile Lys Leu Gly Gln Glu Gln Val Lys Cys Leu Leu Glu  
 1940 1945 1950  
 Ser Leu Pro Ser Asp Phe Ile Pro Lys Ala Gly Ala Leu Ala Leu  
 1955 1960 1965



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<213> NM\_004433 ELF3, E74-like factor 3

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cagcgctacc tggcggaaact ggattttctct cccgcctgcc ggccctgctg ccacagccgg	180
actccgccac tccggtagcc tc atg gct gca acc tgt gag att agc aac att	232
Met Ala Ala Thr Cys Glu Ile Ser Asn Ile	
1 5 10	
ttt agc aac tac ttc agt gcg atg tac agc tcg gag gac tcc acc ctg	280
Phe Ser Asn Tyr Phe Ser Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu	
15 20 25	
gcc tct gtt ccc cct gct gcc acc ttt ggg gcc gat gac ttg gta ctg	328
Ala Ser Val Pro Pro Ala Ala Thr Phe Gly Ala Asp Asp Leu Val Leu	
30 35 40	
acc ctg agc aac ccc cag atg tca ttg gag ggt aca gag aag gcc agc	376
Thr Leu Ser Asn Pro Gln Met Ser Leu Glu Gly Thr Glu Lys Ala Ser	
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tgg ttg ggg gaa cag ccc cag ttc tgg tcg aag acg cag gtt ctg gac	424
Trp Leu Gly Glu Gln Pro Gln Phe Trp Ser Lys Thr Gln Val Leu Asp	
60 65 70	
tgg atc agc tac caa gtg gag aag aac aag tac gac gca agc gcc att	472
Trp Ile Ser Tyr Gln Val Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile	
75 80 85 90	
gac ttc tca cga tgt gac atg gat gcc gcc acc ctc tgc aat tgt gcc	520
Asp Phe Ser Arg Cys Asp Met Asp Gly Ala Thr Leu Cys Asn Cys Ala	
95 100 105	
ctt gag gag ctg cgt ctg gtc ttt ggg cct ctg.ggg gac caa ctc cat	568
Leu Glu Glu Leu Arg Leu Val Phe Gly Pro Leu Gly Asp Gln Leu His	
110 115 120	

gcc cag ctg cga gac ctc act tcc agc tct tct gat gag ctc agt tgg 616  
 Ala Gln Leu Arg Asp Leu Thr Ser Ser Ser Asp Glu Leu Ser Trp  
 125 130 135

atc att gag ctg ctg gag aag gat ggc atg gcc ttc cag gag gcc cta 664  
 Ile Ile Glu Leu Leu Glu Lys Asp Gly Met Ala Phe Gln Glu Ala Leu  
 140 145 150

gac cca ggg ccc ttt gac cag ggc agc ccc ttt gcc cag gag ctg ctg 712  
 Asp Pro Gly Pro Phe Asp Gln Gly Ser Pro Phe Ala Gln Glu Leu Leu  
 155 160 165 170

gac gac ggt cag caa gcc agc ccc tac cac ccc ggc agc tgt ggc gca 760  
 Asp Asp Gly Gln Gln Ala Ser Pro Tyr His Pro Gly Ser Cys Gly Ala  
 175 180 185

gga gcc ccc tcc ccc ggc agc tct gac gtc tcc acc gca ggg act ggt 808  
 Gly Ala Pro Ser Pro Gly Ser Ser Asp Val Ser Thr Ala Gly Thr Gly  
 190 195 200

gct tct cgg agc tcc cac tcc tca gac tcc ggt gga agt gac gtg gac 856  
 Ala Ser Arg Ser Ser His Ser Ser Asp Ser Gly Gly Ser Asp Val Asp  
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ctg gat ccc act gat ggc aag ctc ttc ccc agc gat ggt ttt cgt gac 904  
 Leu Asp Pro Thr Asp Gly Lys Leu Phe Pro Ser Asp Gly Phe Arg Asp  
 220 225 230

tgc aag aag ggg gat ccc aag cac ggg aag cgg aaa cga ggc cgg ccc 952  
 Cys Lys Lys Gly Asp Pro Lys His Gly Lys Arg Lys Arg Gly Arg Pro  
 235 240 245 250

cga aag ctg agc aaa gag tac tgg gac tgt ctc gag ggc aag aag agc 1000  
 Arg Lys Leu Ser Lys Glu Tyr Trp Asp Cys Leu Glu Gly Lys Lys Ser  
 255 260 265

aag cac gcg ccc aga ggc acc cac ctg tgg gag ttc atc cgg gac atc 1048  
 Lys His Ala Pro Arg Gly Thr His Leu Trp Glu Phe Ile Arg Asp Ile  
 270 275 280

ctc atc cac ccg gag ctc aac gag ggc ctc atg aag tgg gag aat cgg 1096  
 Leu Ile His Pro Glu Leu Asn Glu Gly Leu Met Lys Trp Glu Asn Arg  
 285 290 295

cat gaa ggc gtc ttc aag ttc ctg cgc tcc gag gct gtg gcc caa cta 1144  
 His Glu Gly Val Phe Lys Phe Leu Arg Ser Glu Ala Val Ala Gln Leu  
 300 305 310

tgg ggc caa aag aaa aag aac agc aac atg acc tac gag aag ctg agc 1192  
 Trp Gly Gln Lys Lys Lys Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser  
 315 320 325 330

cgg gcc atg agg tac tac tac aaa cgg gag atc ctg gaa cgg gtg gat 1240  
 Arg Ala Met Arg Tyr Tyr Tyr Lys Arg Glu Ile Leu Glu Arg Val Asp  
 335 340 345

ggc cgg cga ctc gtc tac aag ttt ggc aaa aac tca agc ggc tgg aag 1288  
 Gly Arg Arg Leu Val Tyr Lys Phe Gly Lys Asn Ser Ser Gly Trp Lys  
 350 355 360

gag gaa gag gtt ctc cag agt cgg aac tgagggttg aactataccc 1335  
 Glu Glu Glu Val Leu Gln Ser Arg Asn  
 365 370

gggaccaaac tcacggacca ctcgaggcct gcaaacttc ctgggaggac aggcaggcca 1395

gatggcccct ccaactgggga atgctcccag ctgtgctgtg gagagaagct gatgttttgg 1455

tgtattgtca gccatcgicc ttggactcgg agactatggc ctcgcctccc caccctcctc 1515  
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 ttttgcattc cagccaagtg tgctgtaaac tgtatatctg taatatgaat cccagctttt 2475  
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<212> PRT

<213> NM\_004433 ELF3, E74-like factor 3

<400> 40

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20 25 30

Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln  
35 40 45

Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro  
50 55 60

Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val  
65 70 75 80

Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile Asp Phe Ser Arg Cys Asp  
85 90 95

Met Asp Gly Ala Thr Leu Cys Asn Cys Ala Leu Glu Glu Leu Arg Leu  
100 105 110

Val Phe Gly Pro Leu Gly Asp Gln Leu His Ala Gln Leu Arg Asp Leu  
115 120 125

Thr Ser Ser Ser Ser Asp Glu Leu Ser Trp Ile Ile Glu Leu Leu Glu  
130 135 140

Lys Asp Gly Met Ala Phe Gln Glu Ala Leu Asp Pro Gly Pro Phe Asp  
145 150 155 160

Gln Gly Ser Pro Phe Ala Gln Glu Leu Leu Asp Asp Gly Gln Gln Ala  
165 170 175

Ser Pro Tyr His Pro Gly Ser Cys Gly Ala Gly Ala Pro Ser Pro Gly  
180 185 190

Ser Ser Asp Val Ser Thr Ala Gly Thr Gly Ala Ser Arg Ser Ser His  
195 200 205

Ser Ser Asp Ser Gly Gly Ser Asp Val Asp Leu Asp Pro Thr Asp Gly  
210 215 220

Lys Leu Phe Pro Ser Asp Gly Phe Arg Asp Cys Lys Lys Gly Asp Pro  
225 230 235 240

Lys His Gly Lys Arg Lys Arg Gly Arg Pro Arg Lys Leu Ser Lys Glu  
245 250 255

Tyr Trp Asp Cys Leu Glu Gly Lys Lys Ser Lys His Ala Pro Arg Gly  
260 265 270

Thr His Leu Trp Glu Phe Ile Arg Asp Ile Leu Ile His Pro Glu Leu  
275 280 285

Asn Glu Gly Leu Met Lys Trp Glu Asn Arg His Glu Gly Val Phe Lys  
290 295 300

Phe Leu Arg Ser Glu Ala Val Ala Gln Leu Trp Gly Gln Lys Lys Lys  
305 310 315 320

Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser Arg Ala Met Arg Tyr Tyr  
325 330 335

Tyr Lys Arg Glu Ile Leu Glu Arg Val Asp Gly Arg Arg Leu Val Tyr

340

345

350

Lys Phe Gly Lys Asn Ser Ser Gly Trp Lys Glu Glu Glu Val Leu Gln  
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Ser Arg Asn  
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&lt;223&gt;

&lt;400&gt; 41

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 Met Thr Ala Glu Asp Ser Thr Ala Ala Met Ser Ser Asp Ser Ala Ala  
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 ggg tcc tcg gcc aag gtg ccc gag ggc gtg gcg ggc gcg ccc aac gag 335  
 Gly Ser Ser Ala Lys Val Pro Glu Gly Val Ala Gly Ala Pro Asn Glu  
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 gca gca ctg ctg gcg ctg atg gag cgc acg ggc tac agc atg gtg caa 383  
 Ala Ala Leu Leu Ala Leu Met Glu Arg Thr Gly Tyr Ser Met Val Gln  
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 gag aac ggg cag cgc aag tac ggc ggc cca ccg ccc ggc tgg gag ggc 431  
 Glu Asn Gly Gln Arg Lys Tyr Gly Gly Pro Pro Pro Gly Trp Glu Gly  
 50 55 60  
 ccg cac ccg cag cgt ggc tgc gag gtc ttc gtg ggc aag atc ccg cgc 479  
 Pro His Pro Gln Arg Gly Cys Glu Val Phe Val Gly Lys Ile Pro Arg  
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 gac gtg tac gag gac gag ctg gtg ccc gtg ttc gag gcc gtg ggc cgc 527  
 Asp Val Tyr Glu Asp Glu Leu Val Pro Val Phe Glu Ala Val Gly Arg  
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 Thr Tyr Glu Leu Arg Leu Met Met Asp Phe Asp Gly Lys Asn Arg Gly  
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tac gcc ttc gtc atg tac tgc cac aag cac gag gcc aag cgc gca gtg Tyr Ala Phe Val Met Tyr Cys His Lys His Glu Ala Lys Arg Ala Val 115 120 125	623
cgt gag ctc aac aac tac gag atc cgc ccg ggc cgc ctg ctc ggc gtg Arg Glu Leu Asn Asn Tyr Glu Ile Arg Pro Gly Arg Leu Leu Gly Val 130 135 140	671
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cag atc gcc gtg gac tgg gcc gag cct gag atc gac gtg gac gag gac Gln Ile Ala Val Asp Trp Ala Glu Pro Glu Ile Asp Val Asp Glu Asp 225 230 235 240	959
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acc acc gag gac acc atc aag aag agc ttc ggc cag ttc aac ccc ggc Thr Thr Glu Asp Thr Ile Lys Lys Ser Phe Gly Gln Phe Asn Pro Gly 260 265 270	1055
tgc gtg gag cgc gtc aag aag atc cgc gac tac gcc ttc gtg cac ttc Cys Val Glu Arg Val Lys Lys Ile Arg Asp Tyr Ala Phe Val His Phe 275 280 285	1103
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gag ctg gag ggc tcg tgc ctg gag gtc acg ctg gcc aag ccc gtg gac Glu Leu Glu Gly Ser Cys Leu Glu Val Thr Leu Ala Lys Pro Val Asp 305 310 315 320	1199
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aca ctg gcc tac tac ggc tac ccc tac aac gcg ctc att ggg ccc aac Thr Leu Ala Tyr Tyr Gly Tyr Pro Tyr Asn Ala Leu Ile Gly Pro Asn 355 360 365	1343
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tcc atg ttt cca gca gct cca gcc cct aaa atg att gaa gat ggc aaa	1439
Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met Ile Glu Asp Gly Lys	
385 390 395 400	
atc cac aca gtg gag cac atg atc agc ccc att gct gtg cag cca gac	1487
Ile His Thr Val Glu His Met Ile Ser Pro Ile Ala Val Gln Pro Asp	
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Pro Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala	
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Ala Val Ile Pro Thr Val Ser Thr Pro Pro Pro Phe Gln Gly Arg Pro	
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Ile Thr Pro Val Tyr Thr Val Ala Pro Asn Val Gln Arg Ile Pro Thr	
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Ala Gly Ile Tyr Gly Ala Ser Tyr Val Pro Phe Ala Ala Pro Ala Thr	
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Ala Thr Ile Ala Thr Leu Gln Lys Asn Ala Ala Ala Ala Ala Val	
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Tyr Gly Gly Tyr Ala Gly Tyr Ile Pro Gln Ala Phe Pro Ala Ala Ala	
500 505 510	
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Ile Gln Val Pro Ile Pro Asp Val Tyr Gln Thr Tyr	
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&lt;210&gt; 42

&lt;211&gt; 524

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&lt;213&gt; NM\_019027 FLJ20273

&lt;400&gt; 42

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 20 25 30

Ala Ala Leu Leu Ala Leu Met Glu Arg Thr Gly Tyr Ser Met Val Gln  
 35 40 45

Glu Asn Gly Gln Arg Lys Tyr Gly Gly Pro Pro Pro Gly Trp Glu Gly



117

50

55

60

Pro His Pro Gln Arg Gly Cys Glu Val Phe Val Gly Lys Ile Pro Arg  
65 70 75 80

Asp Val Tyr Glu Asp Glu Leu Val Pro Val Phe Glu Ala Val Gly Arg  
85 90 95

Thr Tyr Glu Leu Arg Leu Met Met Asp Phe Asp Gly Lys Asn Arg Gly  
100 105 110

Tyr Ala Phe Val Met Tyr Cys His Lys His Glu Ala Lys Arg Ala Val  
115 120 125

Arg Glu Leu Asn Asn Tyr Glu Ile Arg Pro Gly Arg Leu Leu Gly Val  
130 135 140

Cys Cys Ser Val Asp Asn Cys Arg Leu Phe Ile Gly Gly Ile Pro Lys  
145 150 155 160

Met Lys Lys Arg Glu Glu Ile Leu Glu Glu Ile Ala Lys Val Thr Glu  
165 170 175

Gly Val Leu Asp Val Ile Val Tyr Ala Ser Ala Ala Asp Lys Met Lys  
180 185 190

Asn Arg Gly Phe Ala Phe Val Glu Tyr Glu Ser His Arg Ala Ala Ala  
195 200 205

Met Ala Arg Arg Lys Leu Met Pro Gly Arg Ile Gln Leu Trp Gly His  
210 215 220

Gln Ile Ala Val Asp Trp Ala Glu Pro Glu Ile Asp Val Asp Glu Asp  
225 230 235 240

Val Met Glu Thr Val Lys Ile Leu Tyr Val Arg Asn Leu Met Ile Glu  
245 250 255

Thr Thr Glu Asp Thr Ile Lys Lys Ser Phe Gly Gln Phe Asn Pro Gly  
260 265 270

Cys Val Glu Arg Val Lys Lys Ile Arg Asp Tyr Ala Phe Val His Phe  
275 280 285

Thr Ser Arg Glu Asp Ala Val His Ala Met Asn Asn Leu Asn Gly Thr  
290 295 300

Glu Leu Glu Gly Ser Cys Leu Glu Val Thr Leu Ala Lys Pro Val Asp  
305 310 315 320

Lys Glu Gln Tyr Ser Arg Tyr Gln Lys Ala Ala Arg Gly Gly Gly Ala

325

330

335

Ala Glu Ala Ala Gln Gln Pro Ser Tyr Val Tyr Ser Cys Asp Pro Tyr  
 340 345 350

Thr Leu Ala Tyr Tyr Gly Tyr Pro Tyr Asn Ala Leu Ile Gly Pro Asn  
 355 360 365

Arg Asp Tyr Phe Val Lys Val Ala Ile Pro Ala Ile Gly Ala Gln Tyr  
 370 375 380

Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met Ile Glu Asp Gly Lys  
 385 390 395 400

Ile His Thr Val Glu His Met Ile Ser Pro Ile Ala Val Gln Pro Asp  
 405 410 415

Pro Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala  
 420 425 430

Ala Val Ile Pro Thr Val Ser Thr Pro Pro Pro Phe Gln Gly Arg Pro  
 435 440 445

Ile Thr Pro Val Tyr Thr Val Ala Pro Asn Val Gln Arg Ile Pro Thr  
 450 455 460

Ala Gly Ile Tyr Gly Ala Ser Tyr Val Pro Phe Ala Ala Pro Ala Thr  
 465 470 475 480

Ala Thr Ile Ala Thr Leu Gln Lys Asn Ala Ala Ala Ala Ala Ala Val  
 485 490 495

Tyr Gly Gly Tyr Ala Gly Tyr Ile Pro Gln Ala Phe Pro Ala Ala Ala  
 500 505 510

Ile Gln Val Pro Ile Pro Asp Val Tyr Gln Thr Tyr  
 515 520

&lt;210&gt; 43

&lt;211&gt; 1451

&lt;212&gt; DNA

&lt;213&gt; NM\_013952 PAX8

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (161)..(1354)

&lt;223&gt;

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				Met	Pro	His	Asn	Ser										
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atc	aga	tct	ggc	cat	gga	ggg	ctg	aac	cag	ctg	gga	ggg	gcc	ttt	gtg	223		
Ile	Arg	Ser	Gly	His	Gly	Gly	Leu	Asn	Gln	Leu	Gly	Gly	Ala	Phe	Val			
			10						15					20				
aat	ggc	aga	cct	ctg	ccg	gaa	gtg	gtc	cgc	cag	cgc	atc	gta	gac	ctg	271		
Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln	Arg	Ile	Val	Asp	Leu			
			25					30					35					
gcc	cac	cag	ggt	gta	agg	ccc	tgc	gac	atc	tct	cgc	cag	ctc	cgc	gtc	319		
Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser	Arg	Gln	Leu	Arg	Val			
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agc	cat	ggc	tgc	gtc	agc	aag	atc	ctt	ggc	agg	tac	tac	gag	act	ggc	367		
Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg	Tyr	Tyr	Glu	Thr	Gly			
	55					60					65							
agc	atc	cgg	cct	gga	gtg	ata	ggg	ggc	tcc	aag	ccc	aag	gtg	gcc	acc	415		
Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys	Pro	Lys	Val	Ala	Thr			
70					75					80					85			
ccc	aag	gtg	gtg	gag	aag	att	ggg	gac	tac	aaa	cgc	cag	aac	cct	acc	463		
Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys	Arg	Gln	Asn	Pro	Thr			
				90					95					100				
atg	ttt	gcc	tgg	gag	atc	cga	gac	cgg	ctc	ctg	gct	gag	ggc	gtc	tgt	511		
Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu	Ala	Glu	Gly	Val	Cys			
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gac	aat	gac	act	gtg	ccc	agt	gtc	agc	tcc	att	aat	aga	atc	atc	cgg	559		
Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg			
		120					125					130						
acc	aaa	gtg	cag	caa	cca	ttc	aac	ctc	cct	atg	gac	agc	tgc	gtg	gcc	607		
Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	Asp	Ser	Cys	Val	Ala			
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Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val			
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act	ccc	ccg	gag	tca	ccc	cag	tcg	gat	tcc	ctg	ggc	tcc	acc	tac	tcc	703		
Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser			
			170					175						180				
atc	aat	ggg	ctc	ctg	ggc	atc	gct	cag	cct	ggc	agc	gac	aag	agg	aaa	751		
Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys			
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120

cag cac cac ctc gag ccg ctc gag tgc cca ttt gag cgg cag cac tac 895  
 Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr  
 230 235 240 245  
 cca gag gcc tat gcc tcc ccc agc cac acc aaa ggc gag cag ggc ctc 943  
 Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu  
 250 255 260  
 tac ccg ctg ccc ttg ctc aac agc acc ctg gac gac ggg aag gcc acc 991  
 Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr  
 265 270 275  
 ctg acc cct tcc aac acg cca ctg ggg cgc aac ctc tcg act cac cag 1039  
 Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln  
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 Gly Pro Arg Cys Pro Asp Thr His Pro Thr Ser Pro Pro Ala Asp Arg  
 345 350 355  
 gca gct atg cct cct ctg cca tcg cag gca tgg tgg cag gaa gtg aat 1279  
 Ala Ala Met Pro Pro Leu Pro Ser Gln Ala Trp Trp Gln Glu Val Asn  
 360 365 370  
 act ctg gca atg cct atg gcc aca ccc cct act cct cct aca gcg agg 1327  
 Thr Leu Ala Met Pro Met Ala Thr Pro Pro Thr Pro Pro Thr Ala Arg  
 375 380 385  
 cct ggg gct tcc cca act cca gct tgc tgagttcccc atattattac 1374  
 Pro Gly Ala Ser Pro Thr Pro Ala Cys  
 390 395  
 agttccacat caaggccgag tgcaccgccc accactgcc aaggcctttga ccatctgtag 1434  
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&lt;210&gt; 44

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; NM\_013952 PAX8

&lt;400&gt; 44

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Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
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Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser

35

40

45

Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
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Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80

Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95

Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110

Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125

Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140

Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160

Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175

Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190

Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205

Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220

Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
225 230 235 240

Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
245 250 255

Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
260 265 270

Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn  
275 280 285

Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Ala Pro Pro Phe Trp  
290 295 300

Ile Cys Ser Lys Ser Ala Pro Gly Ser Arg Pro Ser Met Pro Phe Pro  
 305 310 315 320

Met Leu Pro Pro Cys Thr Gly Ser Ser Arg Ala Arg Pro Ser Ser Gln  
 325 330 335

Gly Glu Arg Trp Trp Gly Pro Arg Cys Pro Asp Thr His Pro Thr Ser  
 340 345 350

Pro Pro Ala Asp Arg Ala Ala Met Pro Pro Leu Pro Ser Gln Ala Trp  
 355 360 365

Trp Gln Glu Val Asn Thr Leu Ala Met Pro Met Ala Thr Pro Pro Thr  
 370 375 380

Pro Pro Thr Ala Arg Pro Gly Ala Ser Pro Thr Pro Ala Cys  
 385 390 395

<210> 45

<211> 326

<212> DNA

<213> AI301558 EST

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 gcagggtggtt gcggtcacia agagaaatca tcaagaatgt tcacttggca tgtgtgaaag 180  
 attcaggggg tctgcagctg tttagtgttg atgcagttgg gtcaaaagag tatcatgtta 240  
 gtcttctgtg gggttttaggg agggattatg gagcctccct cccacccac tggctttctt 300  
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<212> DNA

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<220>

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<222> (267)..(938)

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 gtgatgcgcg cggaccagcc cgcgacgccc gggctgccgc tgtccccgca cctggacgct 180  
 ggcgcggtgg ccgcgccccca gctcgatecg ctgcgcgagg cgactcggcc ccaggcttcc 240  
 ggcgcggtg ggggccctcg ctctcc atg ggg ctg agg gac tgg ctg aga acc 293  
 Met Gly Leu Arg Asp Trp Leu Arg Thr  
 1 5  
 gtg tgc tgc tgc tgc cgg tgc gag tgc ttg gag gag cgc gcc ctg cct 341  
 Val Cys Cys Cys Cys Arg Cys Glu Cys Leu Glu Glu Arg Ala Leu Pro  
 10 15 20 25  
 gag aag gag ccc ctc gtc agt gat aac aat cca tat tcc tca ttt gga 389  
 Glu Lys Glu Pro Leu Val Ser Asp Asn Asn Pro Tyr Ser Ser Phe Gly  
 30 35 40  
 gca act ctg gtg agg gat gat gag aag aat tta tgg agt atg ccc cat 437  
 Ala Thr Leu Val Arg Asp Asp Glu Lys Asn Leu Trp Ser Met Pro His  
 45 50 55  
 gat gtg tcc cac aca gag gca gac gac gac aga acc ctg tac aat ttg 485  
 Asp Val Ser His Thr Glu Ala Asp Asp Asp Arg Thr Leu Tyr Asn Leu  
 60 65 70  
 ata gtc att cgt aat cag cag gcc aaa gac tca gag gag tgg cag aag 533  
 Ile Val Ile Arg Asn Gln Gln Ala Lys Asp Ser Glu Glu Trp Gln Lys  
 75 80 85  
 ctc aac tat gat atc cat acc ctg cgg cag gtt cga agg gaa gta aga 581  
 Leu Asn Tyr Asp Ile His Thr Leu Arg Gln Val Arg Arg Glu Val Arg  
 90 95 100 105  
 aac aga tgg aag tgc atc tta gaa gat tta ggt ttt caa aag gaa gct 629  
 Asn Arg Trp Lys Cys Ile Leu Glu Asp Leu Gly Phe Gln Lys Glu Ala  
 110 115 120  
 gac tct ttg ttg tca gtg act aaa ctc agc acc atc agt gat tct aaa 677  
 Asp Ser Leu Leu Ser Val Thr Lys Leu Ser Thr Ile Ser Asp Ser Lys  
 125 130 135  
 aac aca agg aaa gct cga gag atg ttg tta aaa ctg gct gaa gaa acc 725  
 Asn Thr Arg Lys Ala Arg Glu Met Leu Leu Lys Leu Ala Glu Glu Thr  
 140 145 150  
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 Ser Ile Phe Pro Thr Ser Trp Glu Leu Ser Glu Arg Tyr Leu Phe Val  
 155 160 165  
 gtg gac cgt ctc att gca ctt gat gct gca gaa gag ttc ttt aag ctt 821  
 Val Asp Arg Leu Ile Ala Leu Asp Ala Ala Glu Glu Phe Phe Lys Leu  
 170 175 180 185  
 gct cgt cga act tac ccc aag aag cct ggg gtt cca tgc ctg gca gat 869  
 Ala Arg Arg Thr Tyr Pro Lys Lys Pro Gly Val Pro Cys Leu Ala Asp  
 190 195 200  
 ggc cag aaa gaa ctg cac ctg tgg ggg gac ctc tca tgc aga ctt gca 917  
 Gly Gln Lys Glu Leu His Leu Trp Gly Asp Leu Ser Cys Arg Leu Ala  
 205 210 215  
 cat atg cag gga gta ttg cac tgaagatctt tgctggacct tcttctcttc 968

His Met Gln Gly Val Leu His  
220

agaagataat tttcaaaagg gagcaatgct gtgaatgcag cttgcttctc tctacagatt 1028  
gagaagtcca gcttcaaaag ttacttgcca cttaagcaag gaacttgtca agagatcatg 1088  
gttcatgtta ctgaaaagac ttttaaggatt tgtaaggtta atccatagat tgotgagaac 1148  
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<211> 224

<212> PRT

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<400> 47

Met Gly Leu Arg Asp Trp Leu Arg Thr Val Cys Cys Cys Cys Arg Cys  
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20 25 30

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35 40 45

Glu Lys Asn Leu Trp Ser Met Pro His Asp Val Ser His Thr Glu Ala  
50 55 60

Asp Asp Asp Arg Thr Leu Tyr Asn Leu Ile Val Ile Arg Asn Gln Gln  
65 70 75 80

Ala Lys Asp Ser Glu Glu Trp Gln Lys Leu Asn Tyr Asp Ile His Thr  
85 90 95

Leu Arg Gln Val Arg Arg Glu Val Arg Asn Arg Trp Lys Cys Ile Leu  
100 105 110

Glu Asp Leu Gly Phe Gln Lys Glu Ala Asp Ser Leu Leu Ser Val Thr  
115 120 125



125

Lys Leu Ser Thr Ile Ser Asp Ser Lys Asn Thr Arg Lys Ala Arg Glu  
130 135 140

Met Leu Leu Lys Leu Ala Glu Glu Thr Ser Ile Phe Pro Thr Ser Trp  
145 150 155 160

Glu Leu Ser Glu Arg Tyr Leu Phe Val Val Asp Arg Leu Ile Ala Leu  
165 170 175

Asp Ala Ala Glu Glu Phe Phe Lys Leu Ala Arg Arg Thr Tyr Pro Lys  
180 185 190

Lys Pro Gly Val Pro Cys Leu Ala Asp Gly Gln Lys Glu Leu His Leu  
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Trp Gly Asp Leu Ser Cys Arg Leu Ala His Met Gln Gly Val Leu His  
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<211> 2385

<212> DNA

<213> NM\_144724 FLJ30532

<220>

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<222> (71)..(1441)

<223>

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aaaatcacaa atg tca aat gat gga aga tcc agg aat cgg gac agg cgc 109  
Met Ser Asn Asp Gly Arg Ser Arg Asn Arg Asp Arg Arg  
1 5 10

tac gat gag gtc cca agc gac ctg ccc tat caa gat acc acc ata aga 157  
Tyr Asp Glu Val Pro Ser Asp Leu Pro Tyr Gln Asp Thr Thr Ile Arg  
15 20 25

acc cac cca att ctt cat gac agt gag cgg gca gtg agc gct gat ccc 205  
Thr His Pro Ile Leu His Asp Ser Glu Arg Ala Val Ser Ala Asp Pro  
30 35 40 45

ttg cca cca ccc cct ctc cca tta cag cca cca ttc ggc cca gac ttc 253  
Leu Pro Pro Pro Pro Leu Pro Leu Gln Pro Pro Phe Gly Pro Asp Phe  
50 55 60

tac tca agt gac aca gaa gaa cca gct ata gcg cca gat ctc aaa cca 301  
Tyr Ser Ser Asp Thr Glu Glu Pro Ala Ile Ala Pro Asp Leu Lys Pro  
65 70 75

gta agg cgc ttt gtc cct gac tcc tgg aag aac ttt ttc aga ggg aag 349

Val	Arg	Arg	Phe	Val	Pro	Asp	Ser	Trp	Lys	Asn	Phe	Phe	Arg	Gly	Lys	
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aaa	aag	gac	ccc	gaa	tgg	gat	aag	ccg	gtg	tct	gat	atc	agg	tac	atc	397
Lys	Lys	Asp	Pro	Glu	Trp	Asp	Lys	Pro	Val	Ser	Asp	Ile	Arg	Tyr	Ile	
	95					100					105					
tcc	gat	gga	gtg	gag	tgt	tca	cca	cca	gcc	tct	cca	gca	aga	cca	aac	445
Ser	Asp	Gly	Val	Glu	Cys	Ser	Pro	Pro	Ala	Ser	Pro	Ala	Arg	Pro	Asn	
110				115						120					125	
cac	cgt	tcg	ccc	ctc	aac	tcc	tgc	aaa	gat	ccc	tac	gga	ggg	tca	gaa	493
His	Arg	Ser	Pro	Leu	Asn	Ser	Cys	Lys	Asp	Pro	Tyr	Gly	Gly	Ser	Glu	
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gga	acc	ttt	agt	tcc	cgg	aaa	gag	gct	gac	gca	gtg	ttt	ccc	cgg	gat	541
Gly	Thr	Phe		Ser	Arg	Lys	Glu	Ala	Asp	Ala	Val	Phe	Pro	Arg	Asp	
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ccc	tat	gga	tct	cta	gac	cga	cac	aca	caa	aca	gtt	cga	aca	tac	agt	589
Pro	Tyr	Gly	Ser	Leu	Asp	Arg	His	Thr	Gln	Thr	Val	Arg	Thr	Tyr	Ser	
		160					165					170				
gag	aag	gtg	gag	gag	tat	aac	ctg	aga	tac	tcc	tac	atg	aag	tcg	tgg	637
Glu	Lys	Val	Glu	Glu	Tyr	Asn	Leu	Arg	Tyr	Ser	Tyr	Met	Lys	Ser	Trp	
	175					180					185					
gca	ggc	ctg	ctg	aga	ata	ctg	ggg	gtg	gtg	gag	ctg	ctt	ttg	ggg	gcc	685
Ala	Gly	Leu	Leu	Arg	Ile	Leu	Gly	Val	Val	Glu	Leu	Leu	Leu	Gly	Ala	
190					195					200					205	
ggg	gtc	ttt	gct	tgt	gtc	aca	gct	tac	att	cac	aag	gac	agt	gag	tgg	733
Gly	Val	Phe	Ala	Cys	Val	Thr	Ala	Tyr	Ile	His	Lys	Asp	Ser	Glu	Trp	
				210					215					220		
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Tyr	Asn	Leu		Phe	Gly	Tyr	Ser	Gln	Pro	Tyr	Gly	Met	Gly	Gly	Val	
			225					230					235			
gga	ttg	ggc	agt	atg	tat	ggg	ggc	tat	tac	tac	act	ggc	cct	aag	acc	829
Gly	Leu	Gly	Ser	Met	Tyr	Gly	Gly	Tyr	Tyr	Tyr	Thr	Gly	Pro	Lys	Thr	
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Pro	Phe	Val	Leu	Val	Val	Ala	Gly	Leu	Ala	Trp	Ile	Thr	Thr	Ile	Ile	
	255					260					265					
att	ctg	gtt	ctt	ggc	atg	tcc	atg	tat	tac	cgg	acc	att	ctt	ctg	gac	925
Ile	Leu	Val	Leu	Gly	Met	Ser	Met	Tyr	Tyr	Arg	Thr	Ile	Leu	Leu	Asp	
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Ser	Asn	Trp	Trp	Pro	Leu	Thr	Glu	Phe	Gly	Ile	Asn	Val	Ala	Leu	Phe	
				290					295					300		
att	ttg	tat	atg	gcc	gca	gcc	ata	gtc	tat	gtg	aat	gat	acc	aac	cga	1021
Ile	Leu	Tyr	Met	Ala	Ala	Ala	Ile	Val	Tyr	Val	Asn	Asp	Thr	Asn	Arg	
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ggg	ggc	ctc	tgc	tac	tat	ccg	tta	ttt	aat	aca	cca	gtg	aat	gca	gtg	1069
Gly	Gly	Leu	Cys	Tyr	Tyr	Pro	Leu	Phe	Asn	Thr	Pro	Val	Asn	Ala	Val	
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ttc	tgc	cgg	gta	gaa	gga	gga	cag	ata	gct	gca	atg	atc	ttc	ctg	ttt	1117
Phe	Cys	Arg	Val	Glu	Gly	Gly	Gln	Ile	Ala	Ala	Met	Ile	Phe	Leu	Phe	
	335					340					345					
gtc	acc	atg	ata	gtt	tat	ctc	att	agt	gct	ttg	gtt	tgc	cta	aag	tta	1165

Val Thr Met Ile Val Tyr Leu Ile Ser Ala Leu Val Cys Leu Lys Leu	
350 355 360 365	
tgg agg cat gag gca gct cgg aga cat aga gaa tat atg gaa caa cag	1213
Trp Arg His Glu Ala Ala Arg Arg His Arg Glu Tyr Met Glu Gln Gln	
370 375 380	
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Glu Ile Asn Glu Pro Ser Leu Ser Ser Lys Arg Lys Met Cys Glu Met	
385 390 395	
gcc acc agt ggt gac aga caa aga gac tca gaa gtt aat ttc aag gaa	1309
Ala Thr Ser Glu Gly Asp Arg Gln Arg Asp Ser Glu Val Asn Phe Lys Glu	
400 405 410	
ctg aga aca gca aaa atg aaa cct gaa cta ctg agt gga cac atc ccc	1357
Leu Arg Thr Ala Lys Met Lys Pro Glu Leu Leu Ser Gly His Ile Pro	
415 420 425	
cca cgc cca gct aat ttt ttt gta ttt tta gta gag atg ggg ttt cac	1405
Pro Arg Pro Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His	
430 435 440 445	
cgt gtt agc cag gat gat ctc gat ctc ctg acc tca tgatccaccc	1451
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cttttctatt ccctttggac atacatgcta cagtcccaaca atgtagcatt tccttgga	1571
ctccctttttt tttttttttt gagatggagt ttctgtctttg ttgcccaggc tggagtacag	1631
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gcagggatgc ttcattcttc taagaattat cttggctttg gactttattc ataaatgttt	1931
tattttctgtt agtatgaaca atagactgcc ttaacaaagt ttttttttaa acaaaatcgt	1991
tcttgttgga ttttattcag cagcatctat catgtagata aattcccagg tgtagcatta	2051
cagcttctga ctaatatagc tgccattcag acaattaatg ttcaaagagt tttctaaagt	2111
gataaaacca aagaaaagca tgtggaaaag cagaagctta gaaagttgtg gtcactgaat	2171
gcactccctg gtttttattt gtcagtgaat tctttatgca ttcattgtta atattttaat	2231
tccatggcct tgtaggctgt gctgtgtctg aaggggtaac acctagggaa acatgaggcc	2291
ccttatggga ccccccaat ggaacaactt cactttctct tttatgtatt gagccctgtg	2351
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&lt;210&gt; 49

&lt;211&gt; 457

&lt;212&gt; PRT

&lt;213&gt; NM\_144724 FLJ30532

&lt;400&gt; 49

Met Ser Asn Asp Gly Arg Ser Arg Asn Arg Asp Arg Arg Tyr Asp Glu  
1 5 10 15

Val Pro Ser Asp Leu Pro Tyr Gln Asp Thr Thr Ile Arg Thr His Pro  
20 25 30

Ile Leu His Asp Ser Glu Arg Ala Val Ser Ala Asp Pro Leu Pro Pro  
35 40 45

Pro Pro Leu Pro Leu Gln Pro Pro Phe Gly Pro Asp Phe Tyr Ser Ser  
50 55 60

Asp Thr Glu Glu Pro Ala Ile Ala Pro Asp Leu Lys Pro Val Arg Arg  
65 70 75 80

Phe Val Pro Asp Ser Trp Lys Asn Phe Phe Arg Gly Lys Lys Lys Asp  
85 90 95

Pro Glu Trp Asp Lys Pro Val Ser Asp Ile Arg Tyr Ile Ser Asp Gly  
100 105 110

Val Glu Cys Ser Pro Pro Ala Ser Pro Ala Arg Pro Asn His Arg Ser  
115 120 125

Pro Leu Asn Ser Cys Lys Asp Pro Tyr Gly Gly Ser Glu Gly Thr Phe  
130 135 140

Ser Ser Arg Lys Glu Ala Asp Ala Val Phe Pro Arg Asp Pro Tyr Gly  
145 150 155 160

Ser Leu Asp Arg His Thr Gln Thr Val Arg Thr Tyr Ser Glu Lys Val  
165 170 175

Glu Glu Tyr Asn Leu Arg Tyr Ser Tyr Met Lys Ser Trp Ala Gly Leu  
180 185 190

Leu Arg Ile Leu Gly Val Val Glu Leu Leu Leu Gly Ala Gly Val Phe  
195 200 205

Ala Cys Val Thr Ala Tyr Ile His Lys Asp Ser Glu Trp Tyr Asn Leu  
210 215 220

Phe Gly Tyr Ser Gln Pro Tyr Gly Met Gly Gly Val Gly Gly Leu Gly  
225 230 235 240

Ser Met Tyr Gly Gly Tyr Tyr Tyr Thr Gly Pro Lys Thr Pro Phe Val  
245 250 255

Leu Val Val Ala Gly Leu Ala Trp Ile Thr Thr Ile Ile Ile Leu Val  
260 265 270

Leu Gly Met Ser Met Tyr Tyr Arg Thr Ile Leu Leu Asp Ser Asn Trp  
275 280 285

Trp Pro Leu Thr Glu Phe Gly Ile Asn Val Ala Leu Phe Ile Leu Tyr  
290 295 300

Met Ala Ala Ala Ile Val Tyr Val Asn Asp Thr Asn Arg Gly Gly Leu  
305 310 315 320

Cys Tyr Tyr Pro Leu Phe Asn Thr Pro Val Asn Ala Val Phe Cys Arg  
325 330 335

Val Glu Gly Gly Gln Ile Ala Ala Met Ile Phe Leu Phe Val Thr Met  
340 345 350

Ile Val Tyr Leu Ile Ser Ala Leu Val Cys Leu Lys Leu Trp Arg His  
355 360 365

Glu Ala Ala Arg Arg His Arg Glu Tyr Met Glu Gln Gln Glu Ile Asn  
370 375 380

Glu Pro Ser Leu Ser Ser Lys Arg Lys Met Cys Glu Met Ala Thr Ser  
385 390 395 400

Gly Asp Arg Gln Arg Asp Ser Glu Val Asn Phe Lys Glu Leu Arg Thr  
405 410 415

Ala Lys Met Lys Pro Glu Leu Leu Ser Gly His Ile Pro Pro Arg Pro  
420 425 430

Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His Arg Val Ser  
435 440 445

Gln Asp Asp Leu Asp Leu Leu Thr Ser  
450 455

<210> 50

<211> 2280

<212> DNA

<213> NM\_006424 SLC34A2

<220>

<221> CDS

&lt;222&gt; (64)..(2133)

&lt;223&gt;

&lt;400&gt; 50

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 acc atg gct ccc tgg cct gaa ttg gga gat gcc cag ccc aac ccc gat 108  
 Met Ala Pro Trp Pro Glu Leu Gly Asp Ala Gln Pro Asn Pro Asp  
 1 5 10 15  
 aag tac ctc gaa ggg gcc gca ggt cag cag ccc act gcc cct gat aaa 156  
 Lys Tyr Leu Glu Gly Ala Ala Gly Gln Gln Pro Thr Ala Pro Asp Lys  
 20 25 30  
 agc aaa gag acc aac aaa aca gat aac act gag gca cct gta acc aag 204  
 Ser Lys Glu Thr Asn Lys Thr Asp Asn Thr Glu Ala Pro Val Thr Lys  
 35 40 45  
 att gaa ctt ctg ccg tcc tac tcc acg gct aca ctg ata gat gag ccc 252  
 Ile Glu Leu Leu Pro Ser Tyr Ser Thr Ala Thr Leu Ile Asp Glu Pro  
 50 55 60  
 act gag gtg gat gac ccc tgg aac cta ccc act ctt cag gac tcg ggg 300  
 Thr Glu Val Asp Asp Pro Trp Asn Leu Pro Thr Leu Gln Asp Ser Gly  
 65 70 75  
 atc aag tgg tca gag aga gac acc aaa ggg aag att ctc tgt ttc ttc 348  
 Ile Lys Trp Ser Glu Arg Asp Thr Lys Gly Lys Ile Leu Cys Phe Phe  
 80 85 90 95  
 caa ggg att ggg aga ttg att tta ctt ctc gga ttt ctc tac ttt ttc 396  
 Gln Gly Ile Gly Arg Leu Ile Leu Leu Leu Gly Phe Leu Tyr Phe Phe  
 100 105 110  
 gtg tgc tcc ctg gat att ctt agt agc gcc ttc cag ctg gtt gga gga 444  
 Val Cys Ser Leu Asp Ile Leu Ser Ser Ala Phe Gln Leu Val Gly Gly  
 115 120 125  
 aaa atg gca gga cag ttc ttc agc aac agc tct att atg tcc aac cct 492  
 Lys Met Ala Gly Gln Phe Phe Ser Asn Ser Ser Ile Met Ser Asn Pro  
 130 135 140  
 ttg ttg ggg ctg gtg atc ggg gtg ctg gtg acc gtc ttg gtg cag agc 540  
 Leu Leu Gly Leu Val Ile Gly Val Leu Val Thr Val Leu Val Gln Ser  
 145 150 155  
 tcc agc acc tca acg tcc atc gtt gtc agc atg gtg tcc tct tca ttg 588  
 Ser Ser Thr Ser Thr Ser Ile Val Val Ser Met Val Ser Ser Ser Leu  
 160 165 170 175  
 ctc act gtt cgg gct gcc atc ccc att atc atg ggg gcc aac att gga 636  
 Leu Thr Val Arg Ala Ala Ile Pro Ile Ile Met Gly Ala Asn Ile Gly  
 180 185 190  
 acg tca atc acc aac act att gtt gcg ctc atg cag gtg gga gat cgg 684  
 Thr Ser Ile Thr Asn Thr Ile Val Ala Leu Met Gln Val Gly Asp Arg  
 195 200 205  
 agt gag ttc aga aga gct ttt gca gga gcc act gtc cat gac ttc ttc 732  
 Ser Glu Phe Arg Arg Ala Phe Ala Gly Ala Thr Val His Asp Phe Phe  
 210 215 220  
 aac tgg ctg tcc gtg ttg gtg ctc ttg ccc gtg gag gtg gcc acc cat 780  
 Asn Trp Leu Ser Val Leu Val Leu Leu Pro Val Glu Val Ala Thr His  
 225 230 235

tac ctc gag atc ata acc cag ctt ata gtg gag agc ttc cac ttc aag Tyr Leu Glu Ile Ile Thr Gln Leu Ile Val Glu Ser Phe His Phe Lys 240 245 250 255	828
aat gga gaa gat gcc cca gat ctt ctg aaa gtc atc act aag ccc ttc Asn Gly Glu Asp Ala Pro Asp Leu Leu Lys Val Ile Thr Lys Pro Phe 260 265 270	876
aca aag ctc att gtc cag ctg gat aaa aaa gtt atc agc caa att gca Thr Lys Leu Ile Val Gln Leu Asp Lys Lys Val Ile Ser Gln Ile Ala 275 280 285	924
atg aac gat gaa aaa gcg aaa aac aag agt ctt gtc aag att tgg tgc Met Asn Asp Glu Lys Ala Lys Asn Lys Ser Leu Val Lys Ile Trp Cys 290 295 300	972
aaa act ttt acc aac aag acc cag att aac gtc act gtt ccc tcg act Lys Thr Phe Thr Asn Lys Thr Gln Ile Asn Val Thr Val Pro Ser Thr 305 310 315	1020
gct aac tgc acc tcc cct tcc ctc tgt tgg acg gat ggc atc caa aac Ala Asn Cys Thr Ser Pro Ser Leu Cys Trp Thr Asp Gly Ile Gln Asn 320 325 330 335	1068
tgg acc atg aag aat gtg acc tac aag gag aac atc gcc aaa tgc cag Trp Thr Met Lys Asn Val Thr Tyr Lys Glu Asn Ile Ala Lys Cys Gln 340 345 350	1116
cat atc ttt gtg aat ttc cac ctc ccg gat ctt gct gtg ggc acc atc His Ile Phe Val Asn Phe His Leu Pro Asp Leu Ala Val Gly Thr Ile 355 360 365	1164
ttg ctc ata ctc tcc ctg ctg gtc ctc tgt ggt tgc ctg atc atg att Leu Leu Ile Leu Ser Leu Leu Val Leu Cys Gly Cys Leu Ile Met Ile 370 375 380	1212
gtc aag atc ctg ggc tct gtg ctc aag ggg cag gtc gcc act gtc atc Val Lys Ile Leu Gly Ser Val Leu Lys Gly Gln Val Ala Thr Val Ile 385 390 395	1260
aag aag acc atc aac act gat ttc ccc ttt ccc ttt gca tgg ttg act Lys Lys Thr Ile Asn Thr Asp Phe Pro Phe Pro Phe Ala Trp Leu Thr 400 405 410 415	1308
ggc tac ctg gcc atc ctc gtc ggg gca ggc atg acc ttc atc gta cag Gly Tyr Leu Ala Ile Leu Val Gly Ala Gly Met Thr Phe Ile Val Gln 420 425 430	1356
agc agc tct gtg ttc acg tcg gcc ttg acc ccc ctg att gga atc ggc Ser Ser Ser Val Phe Thr Ser Ala Leu Thr Pro Leu Ile Gly Ile Gly 435 440 445	1404
gtg ata acc att gag agg gct tat cca ctc acg ctg ggc tcc aac atc Val Ile Thr Ile Glu Arg Ala Tyr Pro Leu Thr Leu Gly Ser Asn Ile 450 455 460	1452
ggc acc acc acc acc gcc atc ctg gcc gcc tta gcc agc cct ggc aat Gly Thr Thr Thr Thr Ala Ile Leu Ala Ala Leu Ala Ser Pro Gly Asn 465 470 475	1500
gca ttg agg agt tca ctc cag atc gcc ctg tgc cac ttt ttc ttc aac Ala Leu Arg Ser Ser Leu Gln Ile Ala Leu Cys His Phe Phe Phe Asn 480 485 490 495	1548
atc tcc ggc atc ttg ctg tgg tac ccg atc ccg ttc act cgc ctg ccc Ile Ser Gly Ile Leu Leu Trp Tyr Pro Ile Pro Phe Thr Arg Leu Pro 500 505 510	1596

atc cgc atg gcc aag ggg ctg ggc aac atc tct gcc aag tat cgc tgg 1644  
 Ile Arg Met Ala Lys Gly Leu Gly Asn Ile Ser Ala Lys Tyr Arg Trp  
 515 520 525

ttc gcc gtc ttc tac ctg atc atc ttc ttc ttc ctg atc ccg ctg acg 1692  
 Phe Ala Val Phe Tyr Leu Ile Ile Phe Phe Phe Leu Ile Pro Leu Thr  
 530 535 540

gtg ttt ggc ctc tcg ctg gcc ggc tgg cgg gtg ctg gtt ggt gtc ggg 1740  
 Val Phe Gly Leu Ser Leu Ala Gly Trp Arg Val Leu Val Gly Val Gly  
 545 550 555

gtt ccc gtc gtc ttc atc atc atc ctg gta ctg tgc ctc cga ctc ctg 1788  
 Val Pro Val Val Phe Ile Ile Ile Leu Val Leu Cys Leu Arg Leu Leu  
 560 565 570 575

cag tct cgc tgc cca cgc gtc ctg ccg aag aaa ctc cag aac tgg aac 1836  
 Gln Ser Arg Cys Pro Arg Val Leu Pro Lys Lys Leu Gln Asn Trp Asn  
 580 585 590

ttc ctg ccg ctg tgg atg cgc tcg ctg aag ccc tgg gat gcc gtc gtc 1884  
 Phe Leu Pro Leu Trp Met Arg Ser Leu Lys Pro Trp Asp Ala Val Val  
 595 600 605

tcc aag ttc acc ggc tgc ttc cag atg cgc tgc tgc tac tgc tgc cgc 1932  
 Ser Lys Phe Thr Gly Cys Phe Gln Met Arg Cys Cys Tyr Cys Cys Arg  
 610 615 620

gtg tgc tgc cgc gcg tgc tgc ttg ctg tgt ggc tgc ccc aag tgc tgc 1980  
 Val Cys Cys Arg Ala Cys Cys Leu Leu Cys Gly Cys Pro Lys Cys Cys  
 625 630 635

cgc tgc agc aag tgc tgc gag gac ttg gag gag gcg cag gag ggg cag 2028  
 Arg Cys Ser Lys Cys Cys Glu Asp Leu Glu Glu Ala Gln Glu Gly Gln  
 640 645 650 655

gat gtc cct gtc aag gct cct gag acc ttt gat aac ata acc att agc 2076  
 Asp Val Pro Val Lys Ala Pro Glu Thr Phe Asp Asn Ile Thr Ile Ser  
 660 665 670

aga gag gct cag ggt gag gtc cct gcc tcg gac tca aag acc gaa tgc 2124  
 Arg Glu Ala Gln Gly Glu Val Pro Ala Ser Asp Ser Lys Thr Glu Cys  
 675 680 685

acg gcc ttg taggggacgc ccagattgt cagggatggg gggatggtcc 2173  
 Thr Ala Leu  
 690

ttgagttttg catgctctcc tccctccac ttctgcaccc tttcaccacc tcgaggagat 2233

ttgctcccca ttagcgaatg aaattgatgc agtcctaaaa aaaaaaa 2280

&lt;210&gt; 51

&lt;211&gt; 690

&lt;212&gt; PRT

&lt;213&gt; NM\_006424 SLC34A2

&lt;400&gt; 51

Met Ala Pro Trp Pro Glu Leu Gly Asp Ala Gln Pro Asn Pro Asp Lys  
 1 5 10 15



Tyr Leu Glu Gly Ala Ala Gly Gln Gln Pro Thr Ala Pro Asp Lys Ser  
 20 25 30

Lys Glu Thr Asn Lys Thr Asp Asn Thr Glu Ala Pro Val Thr Lys Ile  
 35 40 45

Glu Leu Leu Pro Ser Tyr Ser Thr Ala Thr Leu Ile Asp Glu Pro Thr  
 50 55 60

Glu Val Asp Asp Pro Trp Asn Leu Pro Thr Leu Gln Asp Ser Gly Ile  
 65 70 75 80

Lys Trp Ser Glu Arg Asp Thr Lys Gly Lys Ile Leu Cys Phe Phe Gln  
 85 90 95

Gly Ile Gly Arg Leu Ile Leu Leu Leu Gly Phe Leu Tyr Phe Phe Val  
 100 105 110

Cys Ser Leu Asp Ile Leu Ser Ser Ala Phe Gln Leu Val Gly Gly Lys  
 115 120 125

Met Ala Gly Gln Phe Phe Ser Asn Ser Ser Ile Met Ser Asn Pro Leu  
 130 135 140

Leu Gly Leu Val Ile Gly Val Leu Val Thr Val Leu Val Gln Ser Ser  
 145 150 155 160

Ser Thr Ser Thr Ser Ile Val Val Ser Met Val Ser Ser Ser Leu Leu  
 165 170 175

Thr Val Arg Ala Ala Ile Pro Ile Ile Met Gly Ala Asn Ile Gly Thr  
 180 185 190

Ser Ile Thr Asn Thr Ile Val Ala Leu Met Gln Val Gly Asp Arg Ser  
 195 200 205

Glu Phe Arg Arg Ala Phe Ala Gly Ala Thr Val His Asp Phe Phe Asn  
 210 215 220

Trp Leu Ser Val Leu Val Leu Leu Pro Val Glu Val Ala Thr His Tyr  
 225 230 235 240

Leu Glu Ile Ile Thr Gln Leu Ile Val Glu Ser Phe His Phe Lys Asn  
 245 250 255

Gly Glu Asp Ala Pro Asp Leu Leu Lys Val Ile Thr Lys Pro Phe Thr  
 260 265 270

Lys Leu Ile Val Gln Leu Asp Lys Lys Val Ile Ser Gln Ile Ala Met

275                      280                      285  
 Asn Asp Glu Lys Ala Lys Asn Lys Ser Leu Val Lys Ile Trp Cys Lys  
 290                      295                      300  
 Thr Phe Thr Asn Lys Thr Gln Ile Asn Val Thr Val Pro Ser Thr Ala  
 305                      310                      315                      320  
 Asn Cys Thr Ser Pro Ser Leu Cys Trp Thr Asp Gly Ile Gln Asn Trp  
 325                      330                      335  
 Thr Met Lys Asn Val Thr Tyr Lys Glu Asn Ile Ala Lys Cys Gln His  
 340                      345                      350  
 Ile Phe Val Asn Phe His Leu Pro Asp Leu Ala Val Gly Thr Ile Leu  
 355                      360                      365  
 Leu Ile Leu Ser Leu Leu Val Leu Cys Gly Cys Leu Ile Met Ile Val  
 370                      375                      380  
 Lys Ile Leu Gly Ser Val Leu Lys Gly Gln Val Ala Thr Val Ile Lys  
 385                      390                      395                      400  
 Lys Thr Ile Asn Thr Asp Phe Pro Phe Pro Phe Ala Trp Leu Thr Gly  
 405                      410                      415  
 Tyr Leu Ala Ile Leu Val Gly Ala Gly Met Thr Phe Ile Val Gln Ser  
 420                      425                      430  
 Ser Ser Val Phe Thr Ser Ala Leu Thr Pro Leu Ile Gly Ile Gly Val  
 435                      440                      445  
 Ile Thr Ile Glu Arg Ala Tyr Pro Leu Thr Leu Gly Ser Asn Ile Gly  
 450                      455                      460  
 Thr Thr Thr Thr Ala Ile Leu Ala Ala Leu Ala Ser Pro Gly Asn Ala  
 465                      470                      475                      480  
 Leu Arg Ser Ser Leu Gln Ile Ala Leu Cys His Phe Phe Phe Asn Ile  
 485                      490                      495  
 Ser Gly Ile Leu Leu Trp Tyr Pro Ile Pro Phe Thr Arg Leu Pro Ile  
 500                      505                      510  
 Arg Met Ala Lys Gly Leu Gly Asn Ile Ser Ala Lys Tyr Arg Trp Phe  
 515                      520                      525  
 Ala Val Phe Tyr Leu Ile Ile Phe Phe Phe Leu Ile Pro Leu Thr Val  
 530                      535                      540  
 Phe Gly Leu Ser Leu Ala Gly Trp Arg Val Leu Val Gly Val Gly Val

545                      550                      555                      560  
 Pro Val Val Phe Ile Ile Ile Leu Val Leu Cys Leu Arg Leu Leu Gln  
                                  565                      570                      575  
 Ser Arg Cys Pro Arg Val Leu Pro Lys Lys Leu Gln Asn Trp Asn Phe  
                                  580                      585                      590  
 Leu Pro Leu Trp Met Arg Ser Leu Lys Pro Trp Asp Ala Val Val Ser  
                                  595                      600                      605  
 Lys Phe Thr Gly Cys Phe Gln Met Arg Cys Cys Tyr Cys Cys Arg Val  
                                  610                      615                      620  
 Cys Cys Arg Ala Cys Cys Leu Leu Cys Gly Cys Pro Lys Cys Cys Arg  
                                  625                      630                      635                      640  
 Cys Ser Lys Cys Cys Glu Asp Leu Glu Glu Ala Gln Glu Gly Gln Asp  
                                  645                      650                      655  
 Val Pro Val Lys Ala Pro Glu Thr Phe Asp Asn Ile Thr Ile Ser Arg  
                                  660                      665                      670  
 Glu Ala Gln Gly Glu Val Pro Ala Ser Asp Ser Lys Thr Glu Cys Thr  
                                  675                      680                      685  
 Ala Leu  
                                  690

<210> 52

<211> 529

<212> DNA

<213> AW959311, DKFZp434J037, EST

<220>

<221> misc\_feature

<222> (393)..(393)

<223> the residue at position 393 is A, T C or G

<400> 52

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caagggggccc agcctcctct ggactccacc ttggacctca gtgactcaga acttctgcct 180

ctaagctgct ctaaagtcca gactatggat gtgttctcta ggccttcagg actctagaat 240

gtccatattt atttttatgt tcttggtttt gtgttttagg aaaagtgaat cttgctgttt 300  
 tcaataatgt gaatgctatg ttctgggaaa atccactatg acatctaagt tttgtgtaca 360  
 gagagatatt ttgcaacta ttccacactt ctncacacaac cccccacact ccaactccaca 420  
 ctcttgagtc tctttaccta atggtctcta cctaattggac cctcgtggcc aaaaagtcca 480  
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<210> 53

<211> 2100

<212> DNA

<213> AF111713 JAM1, junctional adhesion molecule 1

<220>

<221> CDS

<222> (287)..(1183)

<223>

<400> 53

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 cggctoactg caacctctc ctcccagagg tactttctcag cctcttagct ccaactgaga 180  
 acccagccag tcaggaagtc gctacttcgg gaacaccaac caatcagggg gccgtcacct 240  
 gctgaaggag tccttcggcg gctgttgtgt cgggagcctg atcgcg atg ggg aca 295  
 Met Gly Thr  
 1

aag gcg caa gtc gag agg aaa ctg ttg tgc ctc ttc ata ttg gcg atc 343  
 Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile  
 5 10 15

ctg ttg tgc tcc ctg gca ttg ggc agt gtt aca gtg cac tct tct gaa 391  
 Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His Ser Ser Glu  
 20 25 30 35

cct gaa gtc aga att cct gag aat aat cct gtg aag ttg tcc tgt gcc 439  
 Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala  
 40 45 50

tac tcg ggc ttt tct tct ccc cgt gtg gag tgg aag ttt gac caa gga 487  
 Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly  
 55 60 65

gac acc acc aga ctc gtt tgc tat aat aac aag atc aca gct tcc tat 535  
 Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr  
 70 75 80

gag gac cgg gtg acc ttc ttg cca act ggt atc acc ttc aag tcc gtg 583  
 Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val  
 85 90 95

aca cgg gaa gac act ggg aca tac act tgt atg gtc tct gag gaa ggc Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly 100 105 110 115	631
ggc aac agc tat ggg gag gtc aag gtc aag ctc atc gtg ctt gtg cct Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val Leu Val Pro 120 125 130	679
cca tcc aag cct aca gtt aac atc ccc tcc tct gcc acc att ggg aac Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn 135 140 145	727
cgg gca gtg ctg aca tgc tca gaa caa gat ggt tcc cca cct tct gaa Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu 150 155 160	775
tac acc tgg ttc aaa gat ggg ata gtg atg cct acg aat ccc aaa agc Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser 165 170 175	823
acc cgt gcc ttc agc aac tct tcc tat gtc ctg aat ccc aca aca gga Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly 180 185 190 195	871
gag ctg gtc ttt gat ccc ctg tca gcc tct gat act gga gaa tac agc Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser 200 205 210	919
tgt gag gca cgg aat ggg tat ggg aca ccc atg act tca aat gct gtg Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val 215 220 225	967
cgc atg gaa gct gtg gag cgg aat gtg ggg gtc atc gtg gca gcc gtc Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val Ala Ala Val 230 235 240	1015
ctt gta acc ctg att ctc ctg gga atc ttg gtt ttt ggc atc tgg ttt Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe 245 250 255	1063
gcc tat agc cga ggc cac ttt gac aga aca aag aaa ggg act tcg agt Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser 260 265 270 275	1111
aag aag gtg att tac agc cag cct agt gcc cga agt gaa gga gaa ttc Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe 280 285 290	1159
aaa cag acc tcg tca ttc ctg gtg tgagcctggg cggctcaccg cctatcatct Lys Gln Thr Ser Ser Phe Leu Val 295	1213
gcatttgcct tactcaggtg ctactggact ctggcccctg atgtctgtag tttcacagga	1273
tgccattattt gtcttctaca cccacaggg cccctactt cttcggatgt gtttttaata	1333
atgtcagcta tgtgcccacat cctccttcat gccctccctc cctttcctac cactgctgag	1393
tggcctggaa cttgtttaaa gtgtttattc cccatttctt tgagggatca ggaaggaatc	1453
ctgggtatgc cattgacttc ccttctaagt agacagcaaa aatggcgggg gtcgcaggaa	1513
tctgcactca actgccacc tggctggcag ggatctttga ataggtatct tgagcttggt	1573
tctgggctct ttccttgtgt actgacgacc agggccagct gttctagagt gggaattaga	1633
ggctagagcg gctgaaatgg ttgtttggtg atgacaactgg ggtccttcca tctctggggc	1693

ccactctctt ctgtcttccc atgggaagtg ccactgggat ccctctgccc tgtcctcctg 1753  
 aatacaagct gactgacatt gactgtgtct gtggaaaatg ggagctcttg ttgtggagag 1813  
 catagtaaat tttcagagaa cttgaagcga aaaggattta aaaccgctgc tctaaagaaa 1873  
 agaaaaactgg aggctgggag cagtgggtca cgctgtgaat cccagaggct gaggcaggcg 1933  
 gatcacctga ggtcgggagt tctggatcag cctgaccaac atggagaaac cctgctggaa 1993  
 atacagagtt agccaggcat ggtgggtgat gcctgtagtc ccagctgctc aggagcctgg 2053  
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<210> 54

<211> 299

<212> PRT

<213> AF111713 JAM1, junctional adhesion molecule 1

<400> 54

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Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
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Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
290 295

<210> 55

<211> 2154

<212> DNA

<213> NM\_006636 MTHFD2, methylene tetrahydrofolate

<220>

<221> CDS

<222> (77)..(1108)

<223>

<400> 55

atataaccgc gtgcccgcgc cgcgcgcttc cctcccggcg cagtcaccgc cgcggtctat 60

ggctgcgact tctcta atg tct gct ttg gct gcc cgg ctg ctg cag ccc gcg 112  
Met Ser Ala Leu Ala Ala Arg Leu Leu Gln Pro Ala  
1 5 10

cac agc tgc tcc ctt cgc ctt cgc cct ttc cac ctc gcg gca gtt cga 160  
His Ser Cys Ser Leu Arg Leu Arg Pro Phe His Leu Ala Ala Val Arg  
15 20 25

140

aat gaa gct gtt gtc att tct gga agg aaa ctg gcc cag cag atc aag Asn Glu Ala Val Val Ile Ser Gly Arg Lys Leu Ala Gln Gln Ile Lys 30 35 40	208
cag gaa gtg cgg cag gag gta gaa gag tgg gtg gcc tca ggc aac aaa Gln Glu Val Arg Gln Glu Val Glu Glu Trp Val Ala Ser Gly Asn Lys 45 50 55 60	256
cgg cca cac ctg agt gtg atc ctg gtt ggc gag aat cct gca agt cac Arg Pro His Leu Ser Val Ile Leu Val Gly Glu Asn Pro Ala Ser His 65 70 75	304
tcc tat gtc ctc aac aaa acc agg gca gct gca gtt gtg gga atc aac Ser Tyr Val Leu Asn Lys Thr Arg Ala Ala Ala Val Val Gly Ile Asn 80 85 90	352
agt gag aca att atg aaa cca gct tca att tca gag gaa gaa ttg ttg Ser Glu Thr Ile Met Lys Pro Ala Ser Ile Ser Glu Glu Glu Leu Leu 95 100 105	400
aat tta atc aat aaa ctg aat aat gat gat aat gta gat ggc ctc ctt Asn Leu Ile Asn Lys Leu Asn Asn Asp Asp Asn Val Asp Gly Leu Leu 110 115 120	448
gtt cag ttg cct ctt cca gag cat att gat gag aga agg atc tgc aat Val Gln Leu Pro Leu Pro Glu His Ile Asp Glu Arg Arg Ile Cys Asn 125 130 135 140	496
gct gtt tct cca gac aag gat gtt gat ggc ttt cat gta att aat gta Ala Val Ser Pro Asp Lys Asp Val Asp Gly Phe His Val Ile Asn Val 145 150 155	544
gga cga atg tgt ttg gat cag tat tcc atg tta ccg gct act cca tgg Gly Arg Met Cys Leu Asp Gln Tyr Ser Met Leu Pro Ala Thr Pro Trp 160 165 170	592
ggg gtg tgg gaa ata atc aag cga act ggc att cca acc cta ggg aag Gly Val Trp Glu Ile Ile Lys Arg Thr Gly Ile Pro Thr Leu Gly Lys 175 180 185	640
aat gtg gtt gtg gct gga agg tca aaa aac gtt gga atg ccc att gca Asn Val Val Val Ala Gly Arg Ser Lys Asn Val Gly Met Pro Ile Ala 190 195 200	688
atg tta ctg cac aca gat ggg gcg cat gaa cgt ccc gga ggt gat gcc Met Leu Leu His Thr Asp Gly Ala His Glu Arg Pro Gly Gly Asp Ala 205 210 215 220	736
act gtt aca ata tct cat cga tat act ccc aaa gag cag ttg aag aaa Thr Val Thr Ile Ser His Arg Tyr Thr Pro Lys Glu Gln Leu Lys Lys 225 230 235	784
cat aca att ctt gca gat att gta ata tct gct gca ggt att cca aat His Thr Ile Leu Ala Asp Ile Val Ile Ser Ala Ala Gly Ile Pro Asn 240 245 250	832
ctg atc aca gca gat atg atc aag gaa gga gca gca gtc att gat gtg Leu Ile Thr Ala Asp Met Ile Lys Glu Gly Ala Ala Val Ile Asp Val 255 260 265	880
gga ata aat aga gtt cac gat cct gta act gcc aaa ccc aag ttg gtt Gly Ile Asn Arg Val His Asp Pro Val Thr Ala Lys Pro Lys Leu Val 270 275 280	928
gga gat gtg gat ttt gaa gga gtc aga caa aaa gct ggg tat atc act Gly Asp Val Asp Phe Glu Gly Val Arg Gln Lys Ala Gly Tyr Ile Thr 285 290 295 300	976



cca gtt cct gga ggt gtt ggc ccc atg aca gtg gca atg cta atg aag 1024  
 Pro Val Pro Gly Gly Val Gly Pro Met Thr Val Ala Met Leu Met Lys  
                   305                  310                  315

aat acc att att gct gca aaa aag gtg ctg agg ctt gaa gag cga gaa 1072  
 Asn Thr Ile Ile Ala Ala Lys Lys Val Leu Arg Leu Glu Glu Arg Glu  
                   320                  325                  330

gtg ctg aag tct aaa gag ctt ggg gta gcc act aat taactactgt 1118  
 Val Leu Lys Ser Lys Glu Leu Gly Val Ala Thr Asn  
                   335                  340

gtcttctgtg tcacaaacag cactccaggc cagctcaaga agcaaagcag gccaatagaa 1178

atgcaatatt tttaatttat tctactgaaa tgggttaaaa tgatgccttg tatttattga 1238

aagcttaaat ggggtgggtgt ttctgcacat acctctgcag tacctcacca gggagcattc 1298

cagtatcatg cagggtcctg tgatctagcc aggagcagcc attaacctag tgattaatat 1358

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tgccttttcc taggattgca tttcccaagt gctattgcaa taacagttga tactcatttt 1478

aggtaccaga ccttttgagt tcaactgac aaaccaaagg aaaagtgttg ctagagaaaa 1538

ttggggaaaa ggtgaaaaag aaaaaatggt agtaattgag cagaaaaaaa ttaatttata 1598

tatgtattga ttggcaacca gatttatcta agtagaactg aattggctag gaaaaaagaa 1658

aaactgcatg ttaatcattt tcctaagctg tccttttgag gcttagtcag tttattggga 1718

aaatgtttag gattattcct tgctattagt actcatttta tgtatgttac ccttcagtaa 1778

gttctcccca ttttagtttt ctaggactga aaggattcct ttctacatta tacatgtgtg 1838

ttgtcatatt tggcttttgc tatatacttt aacttcattg ttaaattttt gtattgtata 1898

gtttcttttg tgatatctaa aacctatttt tgaaaaacaa acttggttg ataatcattt 1958

gggcagcttg ggtaagtacg caacttactt ttccacaaa gaactgtcag cagctgcctg 2018

cttttctgtg atgtatgtat cctgttgact tttccagaaa ttttttaaga gtttgagtta 2078

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tctgtctggg atggta 2154

&lt;210&gt; 56

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; NM\_006636 MTHFD2, methylene tetrahydrofolate

&lt;400&gt; 56

Met Ser Ala Leu Ala Ala Arg Leu Leu Gln Pro Ala His Ser Cys Ser  
 1                  5                  10                  15

Leu Arg Leu Arg Pro Phe His Leu Ala Ala Val Arg Asn Glu Ala Val  
 20                  25                  30

Val Ile Ser Gly Arg Lys Leu Ala Gln Gln Ile Lys Gln Glu Val Arg  
35 40 45

Gln Glu Val Glu Glu Trp Val Ala Ser Gly Asn Lys Arg Pro His Leu  
50 55 60

Ser Val Ile Leu Val Gly Glu Asn Pro Ala Ser His Ser Tyr Val Leu  
65 70 75 80

Asn Lys Thr Arg Ala Ala Ala Val Val Gly Ile Asn Ser Glu Thr Ile  
85 90 95

Met Lys Pro Ala Ser Ile Ser Glu Glu Glu Leu Leu Asn Leu Ile Asn  
100 105 110

Lys Leu Asn Asn Asp Asp Asn Val Asp Gly Leu Leu Val Gln Leu Pro  
115 120 125

Leu Pro Glu His Ile Asp Glu Arg Arg Ile Cys Asn Ala Val Ser Pro  
130 135 140

Asp Lys Asp Val Asp Gly Phe His Val Ile Asn Val Gly Arg Met Cys  
145 150 155 160

Leu Asp Gln Tyr Ser Met Leu Pro Ala Thr Pro Trp Gly Val Trp Glu  
165 170 175

Ile Ile Lys Arg Thr Gly Ile Pro Thr Leu Gly Lys Asn Val Val Val  
180 185 190

Ala Gly Arg Ser Lys Asn Val Gly Met Pro Ile Ala Met Leu Leu His  
195 200 205

Thr Asp Gly Ala His Glu Arg Pro Gly Gly Asp Ala Thr Val Thr Ile  
210 215 220

Ser His Arg Tyr Thr Pro Lys Glu Gln Leu Lys Lys His Thr Ile Leu  
225 230 235 240

Ala Asp Ile Val Ile Ser Ala Ala Gly Ile Pro Asn Leu Ile Thr Ala  
245 250 255

Asp Met Ile Lys Glu Gly Ala Ala Val Ile Asp Val Gly Ile Asn Arg  
260 265 270

Val His Asp Pro Val Thr Ala Lys Pro Lys Leu Val Gly Asp Val Asp  
275 280 285

Phe Glu Gly Val Arg Gln Lys Ala Gly Tyr Ile Thr Pro Val Pro Gly  
290 295 300

Gly Val Gly Pro Met Thr Val Ala Met Leu Met Lys Asn Thr Ile Ile  
305 310 315 320

Ala Ala Lys Lys Val Leu Arg Leu Glu Glu Arg Glu Val Leu Lys Ser  
325 330 335

Lys Glu Leu Gly Val Ala Thr Asn  
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<210> 57

<211> 1117

<212> DNA

<213> NM\_006149 galectin 4, LGALS4

<220>

<221> CDS

<222> (57)..(1025)

<223>

<400> 57

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Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr Leu  
5 10 15

cct tac tac cag ccc atc ccg ggc ggg ctc aac gtg gga atg tct gtt 155  
Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser Val  
20 25 30

tac atc caa gga gtg gcc agc gag cac atg aag ccg ttc ttc gtg aac 203  
Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val Asn  
35 40 45

ttt gtg gtt ggg cag gat ccg ggc tca gac gtc gcc ttc cac ttc aat 251  
Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe Asn  
50 55 60 65

ccg ccg ttt gac ggc tgg gac aag gtg gtc ttc aac acg ttg cag ggc 299  
Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln Gly  
70 75 80

ggg aag tgg ggc agc gag gag agg aag agg agc atg ccc ttc aaa aag 347  
Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys Lys  
85 90 95

ggt gcc gcc ttt gag ctg gtc ttc ata gtc ctg gct gag cac tac aag 395  
Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr Lys  
100 105 110

gtg gtg gta aat gga aat ccc ttc tat gag tac ggg cac cgg ctt ccc 443  
Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu Pro

115	120	125	
cta cag atg gtc acc cac ctg caa gtg gat ggg gat ctg caa ctt caa Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu Gln 130 135 140 145			491
tca atc aac ttc atc gga ggc cag ccc ctg cgg ccc cag gga ccc ccg Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro Pro 150 155 160			539
atg atg cca cct tac cct ggt ccc gga cat tgc cat caa cag ctg aac Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu Asn 165 170 175			587
agc ctg ccc acc atg gaa gga ccc cca acc ttc aac ccg cct gtg cca Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val Pro 180 185 190			635
tat ttc ggg agg ctg caa gga ggg ctg aca gct cga aga acc atc atc Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile Ile 195 200 205			683
atc aag ggc tat gtg cct ccc aca ggc aag agc ttt gct atc aac ttc Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn Phe 210 215 220 225			731
aag gtg ggc tcc tca ggg gac ata gct ctg cac att aat ccc cgc atg Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg Met 230 235 240			779
ggc aac ggt acc gtg gtc cgg aac agc ctt ctg aat ggc tcg tgg gga Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp Gly 245 250 255			827
tcc gag gag aag aag atc acc cac aac cca ttt ggt ccc gga cag ttc Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln Phe 260 265 270			875
ttt gat ctg tcc att cgc tgt ggc ttg gat cgc ttc aag gtt tac gcc Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr Ala 275 280 285			923
aat ggc cag cac ctg ttt gac ttt gcc cat cgc ctg tcg gcc ttc cag Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe Gln 290 295 300 305			971
agg gtg gac aca ttg gaa atc cag ggt gat gtc acc ttg tcc tat gtc Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr Val 310 315 320			1019
cag atc taatctattc ctggggccat aactcatggg aaaacagaat tatccctag Gln Ile			1075

gactcctttc taagccccta ataaaatgtc tgagggtgtc tc 1117

<210> 58

<211> 323

<212> PRT

<213> NM\_006149 galectin 4, LGALS4

<400> 58

Met Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr  
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Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser  
20 25 30

Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val  
35 40 45

Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe  
50 55 60

Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln  
65 70 75 80

Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys  
85 90 95

Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr  
100 105 110

Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu  
115 120 125

Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu  
130 135 140

Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro  
145 150 155 160

Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu  
165 170 175

Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val  
180 185 190

Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile  
195 200 205

Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn  
210 215 220

Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg  
225 230 235 240

Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp  
245 250 255

Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln  
260 265 270

Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr  
 275 280 285

Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe  
 290 295 300

Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr  
 305 310 315 320

Val Gln Ile

<210> 59

<211> 3697

<212> DNA

<213> NM\_004063 cadherin 17, CDH17

<220>

<221> CDS

<222> (121)..(2616)

<223>

<400> 59  
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 atg ata ctt cag gcc cat ctt cac tcc ctg tgt ctt ctt atg ctt tat 168  
 Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr  
 1 5 10 15  
 ttg gca act gga tat ggc caa gag ggg aag ttt agt gga ccc ctg aaa 216  
 Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys  
 20 25 30  
 ccc atg aca ttt tct att tat gaa ggc caa gaa ccg agt caa att ata 264  
 Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile  
 35 40 45  
 ttc cag ttt aag gcc aat cct cct gct gtg act ttt gaa cta act ggg 312  
 Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly  
 50 55 60  
 gag aca gac aac ata ttt gtg ata gaa cgg gag gga ctt ctg tat tac 360  
 Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr  
 65 70 75 80  
 aac aga gcc ttg gac agg gaa aca aga tct act cac aat ctc cag gtt 408  
 Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val  
 85 90 95  
 gca gcc ctg gac gct aat gga att ata gtg gag ggt cca gtc cct atc 456  
 Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile

100	105	110	
acc ata gaa gtg aag gac atc aac gac aat cga ccc acg ttt ctc cag Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln 115 120 125			504
tca aag tac gaa ggc tca gta agg cag aac tct cgc cca gga aag ccc Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro 130 135 140			552
ttc ttg tat gtc aat gcc aca gac ctg gat gat ccg gcc act ccc aat Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn 145 150 155 160			600
ggc cag ctt tat tac cag att gtc atc cag ctt ccc atg atc aac aat Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn 165 170 175			648
gtc atg tac ttt cag atc aac aac aaa acg gga gcc atc tct ctt acc Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr 180 185 190			696
cga gag gga tct cag gaa ttg aat cct gct aag aat cct tcc tat aat Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn 195 200 205			744
ctg gtg atc tca gtg aag gac atg gga ggc cag agt gag aat tcc ttc Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe 210 215 220			792
agt gat acc aca tct gtg gat atc ata gtg aca gag aat att tgg aaa Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys 225 230 235 240			840
gca cca aaa cct gtg gag atg gtg gaa aac tca act gat cct cac ccc Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro 245 250 255			888
atc aaa atc act cag gtg cgg tgg aat gat ccc ggt gca caa tat tcc Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser 260 265 270			936
tta gtt gac aaa gag aag ctg cca aga ttc cca ttt tca att gac cag Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln 275 280 285			984
gaa gga gat att tac gtg act cag ccc ttg gac cga gaa gaa aag gat Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp 290 295 300			1032
gca tat gtt ttt tat gca gtt gca aag gat gag tac gga aaa cca ctt Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu 305 310 315 320			1080
tca tat ccg ctg gaa att cat gta aaa gtt aaa gat att aat gat aat Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn 325 330 335			1128
cca cct aca tgt ccg tca cca gta acc gta ttt gag gtc cag gag aat Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn 340 345 350			1176
gaa cga ctg ggt aac agt atc ggg acc ctt act gca cat gac agg gat Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp 355 360 365			1224
gaa gaa aat act gcc aac agt ttt cta aac tac agg att gtg gag caa Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln 370 375 380			1272

370	375	380	
act ccc aaa ctt ccc atg gat gga ctc ttc cta atc caa acc tat gct Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala 385 390 395 400			1320
gga atg tta cag tta gct aaa cag tcc ttg aag aag caa gat act cct Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro 405 410 415			1368
cag tac aac tta acg ata gag gtg tct gac aaa gat ttc aag acc ctt Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu 420 425 430			1416
tgt ttt gtg caa atc aac gtt att gat atc aat gat cag atc ccc atc Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile 435 440 445			1464
ttt gaa aaa tca gat tat gga aac ctg act ctt gct gaa gac aca aac Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn 450 455 460			1512
att ggg tcc acc atc tta acc atc cag gcc act gat gct gat gag cca Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro 465 470 475 480			1560
ttt act ggg agt tct aaa att ctg tat cat atc ata aag gga gac agt Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser 485 490 495			1608
gag gga cgc ctg ggg gtt gac aca gat ccc cat acc aac acc gga tat Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr 500 505 510			1656
gtc ata att aaa aag cct ctt gat ttt gaa aca gca gct gtt tcc aac Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn 515 520 525			1704
att gtg ttc aaa gca gaa aat cct gag cct cta gtg ttt ggt gtg aag Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys 530 535 540			1752
tac aat gca agt tct ttt gcc aag ttc acg ctt att gtg aca gat gtg Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val 545 550 555 560			1800
aat gaa gca cct caa ttt tcc caa cac gta ttc caa gcg aaa gtc agt Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser 565 570 575			1848
gag gat gta gct ata ggc act aaa gtg ggc aat gtg act gcc aag gat Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp 580 585 590			1896
cca gaa ggt ctg gac ata agc tat tca ctg agg gga gac aca aga ggt Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly 595 600 605			1944
tgg ctt aaa att gac cac gtg act ggt gag atc ttt agt gtg gct cca Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro 610 615 620			1992
ttg gac aga gaa gcc gga agt cca tat cgg gta caa gtg gtg gcc aca Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr 625 630 635 640			2040
gaa gta ggg ggg tct tcc ttg agc tct gtg tca gag ttc cac ctg atc Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile			2088



645	650	655	
ctt atg gat gtg aat gac aac cct ccc agg cta gcc aag gac tac acg Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr 660 665 670	2136		
ggc ttg ttc ttc tgc cat ccc ctc agt gca cct gga agt ctc att ttc Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe 675 680 685	2184		
gag gct act gat gat gat cag cac tta ttt cgg ggt ccc cat ttt aca Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr 690 695 700	2232		
ttt tcc ctc ggc agt gga agc tta caa aac gac tgg gaa gtt tcc aaa Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys 705 710 715 720	2280		
atc aat ggt act cat gcc cga ctg tct acc agg cac aca gag ttt gag Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Glu Phe Glu 725 730 735	2328		
gag agg gag tat gtc gtc ttg atc cgc atc aat gat ggg ggt cgg cca Glu Arg Glu Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro 740 745 750	2376		
ccc ttg gaa ggc att gtt tct tta cca gtt aca ttc tgc agt tgt gtg Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val 755 760 765	2424		
gaa gga agt tgt ttc cgg cca gca ggt cac cag act ggg ata ccc act Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr 770 775 780	2472		
gtg ggc atg gca gtt ggt ata ctg ctg acc acc ctt ctg gtg att ggt Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly 785 790 795 800	2520		
ata att tta gca gtt gtg ttt atc cgc ata aag aag gat aaa ggc aaa Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys 805 810 815	2568		
gat aat gtt gaa agt gct caa gca tct gaa gtc aaa cct ctg aga agc Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser 820 825 830	2616		
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cctttaatat ttgctaaata tttctttttt gaggtggagt cttgctctgt cgcccaggct	2796		
ggagtacagt ggtgtgatcc cagctcactg caacctccgc ctctggggtt cacatgattc	2856		
tcctgcctca gcttccctaag tagctggggt tacaggcacc caccaccatg ccagactaat	2916		
ttttgtattt ttaatagaga cgggggtttcg ccatttggcc aggctggtct tgaactcctg	2976		
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acttagatat ttcattgtgt atagacatta gagagatttt tcatttttcc atgacatttt	3096		
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taaatattct gtacattttt tctttatcaa ggagatatat cagtgttgct tcatagaact	3216		
gcctggattc cttttatggt ttttctgatt ccactctgtg tccccttcat ccttgactcc	3276		

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tttgggtatct cactgaattt caaacatttg tcagagaaga aaaacgtgag gactcaggaa 3336
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tcattcgatg gttagtaaag ttttgggtat tatatatatta acatgtggaa gaaaacaaga 3636
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a 3697

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&lt;210&gt; 60

&lt;211&gt; 832

&lt;212&gt; PRT

&lt;213&gt; NM\_004063 cadherin 17, CDH17

&lt;400&gt; 60

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Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys
          20           25           30

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Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile
          35           40           45

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Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly
          50           55           60

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Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr
65           70           75           80

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Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val
          85           90           95

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Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile
          100          105          110

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Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln
          115          120          125

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Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro
          130          135          140

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Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn
          145          150          155          160

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Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn  
165 170 175

Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr  
180 185 190

Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn  
195 200 205

Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe  
210 215 220

Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys  
225 230 235 240

Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro  
245 250 255

Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser  
260 265 270

Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln  
275 280 285

Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp  
290 295 300

Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu  
305 310 315 320

Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn  
325 330 335

Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn  
340 345 350

Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp  
355 360 365

Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln  
370 375 380

Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala  
385 390 395 400

Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro  
405 410 415

Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu  
420 425 430

Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile  
 435 440 445  
 Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn  
 450 455 460  
 Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro  
 465 470 475 480  
 Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser  
 485 490 495  
 Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr  
 500 505 510  
 Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn  
 515 520 525  
 Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys  
 530 535 540  
 Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val  
 545 550 555 560  
 Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser  
 565 570 575  
 Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp  
 580 585 590  
 Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly  
 595 600 605  
 Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro  
 610 615 620  
 Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr  
 625 630 635 640  
 Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile  
 645 650 655  
 Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr  
 660 665 670  
 Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe  
 675 680 685  
 Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr  
 690 695 700

Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys  
705 710 715 720

Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Glu Phe Glu  
725 730 735

Glu Arg Glu Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro  
740 745 750

Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val  
755 760 765

Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr  
770 775 780

Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly  
785 790 795 800

Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys  
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Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser  
820 825 830

<210> 61

<211> 2920

<212> DNA

<213> NM\_005588; meprin A, alpha

<220>

<221> CDS

<222> (10)..(2247)

<223>

<400> 61

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ctt ttt gcc cac ata gca gct gta ccg att aag cat ctt cct gaa gaa 99  
Leu Phe Ala His Ile Ala Ala Val Pro Ile Lys His Leu Pro Glu Glu  
15 20 25 30

aat gta cat gat gca gat ttt ggt gaa cag aag gat att tca gaa atc 147  
Asn Val His Asp Ala Asp Phe Gly Glu Gln Lys Asp Ile Ser Glu Ile  
35 40 45

aat tta gct gca ggc ttg gac ctc ttt caa ggg gac atc ctc ttg cag 195  
Asn Leu Ala Ala Gly Leu Asp Leu Phe Gln Gly Asp Ile Leu Leu Gln

50	55	60	
aaa tcc aga aat ggc ctg aga gac cca aac acc agg tgg acg ttc ccc Lys Ser Arg Asn Gly Leu Arg Asp Pro Asn Thr Arg Trp Thr Phe Pro 65 70 75			243
att cct tac atc ttg gct gat aat ttg ggg ctg aat gct aaa gga gcc Ile Pro Tyr Ile Leu Ala Asp Asn Leu Gly Leu Asn Ala Lys Gly Ala 80 85 90			291
att ctg tat gcc ttt gag atg ttc cgt ctc aag tcc tgt gtg gat ttc Ile Leu Tyr Ala Phe Glu Met Phe Arg Leu Lys Ser Cys Val Asp Phe 95 100 105 110			339
aag ccc tat gaa gga gag agc tca tat atc ata ttt caa cag ttt gat Lys Pro Tyr Glu Gly Glu Ser Ser Tyr Ile Ile Phe Gln Gln Phe Asp 115 120 125			387
ggg tgc tgg tct gag gtt ggt gac caa cat gtg gga cag aac att tcc Gly Cys Trp Ser Glu Val Gly Asp Gln His Val Gly Gln Asn Ile Ser 130 135 140			435
att ggc caa gga tgt gcc tat aag gcc atc ata gaa cac gag atc ctg Ile Gly Gln Gly Cys Ala Tyr Lys Ala Ile Ile Glu His Glu Ile Leu 145 150 155			483
cat gct ttg gga ttt tac cac gag cag tca agg acg gac cgg gat gat His Ala Leu Gly Phe Tyr His Glu Gln Ser Arg Thr Asp Arg Asp Asp 160 165 170			531
tat gtg aac atc tgg tgg gac caa att ctt tca ggt tac cag cac aac Tyr Val Asn Ile Trp Trp Asp Gln Ile Leu Ser Gly Tyr Gln His Asn 175 180 185 190			579
ttt gac acc tat gat gat agc tta atc aca gac ctc aat aca ccc tat Phe Asp Thr Tyr Asp Asp Ser Leu Ile Thr Asp Leu Asn Thr Pro Tyr 195 200 205			627
gat tat gag tct ttg atg cac tac cag cct ttc tca ttt aac aag aat Asp Tyr Glu Ser Leu Met His Tyr Gln Pro Phe Ser Phe Asn Lys Asn 210 215 220			675
gca agt gtt ccc acc atc aca gcc aag atc cct gag ttt aac tcc att Ala Ser Val Pro Thr Ile Thr Ala Lys Ile Pro Glu Phe Asn Ser Ile 225 230 235			723
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cga atg tac aat tgc acc aca act cac act ctt ttg gac cac tgt act Arg Met Tyr Asn Cys Thr Thr His Thr Leu Leu Asp His Cys Thr 255 260 265 270			819
ttt gag aag gca aac atc tgt gga atg att cag ggc acc aga gat gac Phe Glu Lys Ala Asn Ile Cys Gly Met Ile Gln Gly Thr Arg Asp Asp 275 280 285			867
act gac tgg gcc cat cag gac agt gct cag gct gga gaa gtg gat cac Thr Asp Trp Ala His Gln Asp Ser Ala Gln Ala Gly Glu Val Asp His 290 295 300			915
acc ttg ttg gga caa tgc aca ggt gcc ggc tac ttc atg cag ttc agc Thr Leu Leu Gly Gln Cys Thr Gly Ala Gly Tyr Phe Met Gln Phe Ser 305 310 315			963
acc agc tcg ggg tcc gcg gaa gag gca gcc cta ctg gag tct cgg att Thr Ser Ser Gly Ser Ala Glu Glu Ala Ala Leu Leu Glu Ser Arg Ile			1011

320	325	330	
ctt tac cca aag agg aag cag cag tgc ctg caa ttt ttc tat aaa atg Leu Tyr Pro Lys Arg Lys Gln Gln Cys Leu Gln Phe Phe Tyr Lys Met 335 340 345 350			1059
acg gga agt cct tca gac aga ctc gtt gtc tgg gtc agg agg gat gac Thr Gly Ser Pro Ser Asp Arg Leu Val Val Trp Val Arg Arg Asp Asp 355 360 365			1107
agc aca ggc aat gtt cgc aag ttg gtg aag gtg cag act ttt caa gga Ser Thr Gly Asn Val Arg Lys Leu Val Lys Val Gln Thr Phe Gln Gly 370 375 380			1155
gat gat gac cac aat tgg aaa att gcc cat gtg gtg ctc aaa gag gaa Asp Asp Asp His Asn Trp Lys Ile Ala His Val Val Leu Lys Glu Glu 385 390 395			1203
cag aag ttt cgc tac ctt ttc cag ggc aca aaa ggc gac cct cag aac Gln Lys Phe Arg Tyr Leu Phe Gln Gly Thr Lys Gly Asp Pro Gln Asn 400 405 410			1251
tca act ggg gga att tac cta gat gac atc act ctg aca gaa acc ccc Ser Thr Gly Gly Ile Tyr Leu Asp Asp Ile Thr Leu Thr Glu Thr Pro 415 420 425 430			1299
tgc ccc aca ggg gtc tgg aca gtc cgg aat ttc tcc caa gtc ctt gag Cys Pro Thr Gly Val Trp Thr Val Arg Asn Phe Ser Gln Val Leu Glu 435 440 445			1347
aac acc agc aaa ggg gac aag ctt cag agc cct cga ttc tac aat tcg Asn Thr Ser Lys Gly Asp Lys Leu Gln Ser Pro Arg Phe Tyr Asn Ser 450 455 460			1395
gag gga tat ggt ttt ggg gta act tta tac cca aat agc aga gaa agc Glu Gly Tyr Gly Phe Gly Val Thr Leu Tyr Pro Asn Ser Arg Glu Ser 465 470 475			1443
tct ggt tac ttg aga ctt gct ttt cat gtg tgc agt ggg gag aac gat Ser Gly Tyr Leu Arg Leu Ala Phe His Val Cys Ser Gly Glu Asn Asp 480 485 490			1491
gct atc ctg gag tgg ccg gta gaa aac aga cag gtg ata att acc atc Ala Ile Leu Glu Trp Pro Val Glu Asn Arg Gln Val Ile Ile Thr Ile 495 500 505 510			1539
ctt gac cag gag cct gat gtc cgg aac agg atg tcc tca agc atg gtg Leu Asp Gln Glu Pro Asp Val Arg Asn Arg Met Ser Ser Ser Met Val 515 520 525			1587
ttc act acc tcg aag tcg cac aca tct cca gcg ata aat gac act gtc Phe Thr Thr Ser Lys Ser His Thr Ser Pro Ala Ile Asn Asp Thr Val 530 535 540			1635
atc tgg gac agg ccg tcc agg gtg gga acc tat cat aca gac tgt aat Ile Trp Asp Arg Pro Ser Arg Val Gly Thr Tyr His Thr Asp Cys Asn 545 550 555			1683
tgt ttt aga agc atc gac ttg ggc tgg agt ggt ttc att tcc cac caa Cys Phe Arg Ser Ile Asp Leu Gly Trp Ser Gly Phe Ile Ser His Gln 560 565 570			1731
atg ctg aaa agg agg agt ttc ctg aaa aat gat gac ctc atc ata ttt Met Leu Lys Arg Arg Ser Phe Leu Lys Asn Asp Asp Leu Ile Ile Phe 575 580 585 590			1779
gtg gac ttt gaa gat atc acc cac ctc agc cag act gaa gtt ccc tct Val Asp Phe Glu Asp Ile Thr His Leu Ser Gln Thr Glu Val Pro Ser 600 605 610			1827

595	600	605	
aaa ggc aaa aga ctg agc ccc caa ggc ctc att ctc caa ggc cag gag Lys Gly Lys Arg Leu Ser Pro Gln Gly Leu Ile Leu Gln Gly Gln Glu 610 615 620			1875
cag cag gtc tcc gaa gaa ggt tgc gga aag gcc atg tta gag gaa gcc Gln Gln Val Ser Glu Glu Gly Ser Gly Lys Ala Met Leu Glu Glu Ala 625 630 635			1923
cta cct gtc agc ctg agc cag ggg cag ccc agc cga cag aag cgg tgc Leu Pro Val Ser Leu Ser Gln Gly Gln Pro Ser Arg Gln Lys Arg Ser 640 645 650			1971
gtg gag aac aca ggc ccc ctg gag gac cat aac tgg cca cag tac ttc Val Glu Asn Thr Gly Pro Leu Glu Asp His Asn Trp Pro Gln Tyr Phe 655 660 665 670			2019
aga gac cca tgt gac cca aac cct tgc caa aat gac ggc atc tgt gtg Arg Asp Pro Cys Asp Pro Asn Pro Cys Gln Asn Asp Gly Ile Cys Val 675 680 685			2067
aac gtg aag ggg atg gcg agc tgc agg tgc atc tct gga cat gct ttc Asn Val Lys Gly Met Ala Ser Cys Arg Cys Ile Ser Gly His Ala Phe 690 695 700			2115
ttc tac acg ggg gag cgc tgt cag tgc gcc gag gtg cac ggc agt gtc Phe Tyr Thr Gly Glu Arg Cys Gln Ser Ala Glu Val His Gly Ser Val 705 710 715			2163
ctg ggc atg gtg atc gga ggc acg gct ggc gtg atc ttc ttg acc ttc Leu Gly Met Val Ile Gly Gly Thr Ala Gly Val Ile Phe Leu Thr Phe 720 725 730			2211
tcc atc atc gcc atc ctt tcc caa agg cca agg aag tgacctgcct Ser Ile Ile Ala Ile Leu Ser Gln Arg Pro Arg Lys 735 740 745			2257
gctggcattg gccagaccac agcagcacct cctccatgca ggccttaact ttcccatggt			2317
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aaa			2920

&lt;210&gt; 62

&lt;211&gt; 746



&lt;212&gt; PRT

&lt;213&gt; NM\_005588; meprin A, alpha

&lt;400&gt; 62

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 20 25 30

His Asp Ala Asp Phe Gly Glu Gln Lys Asp Ile Ser Glu Ile Asn Leu  
 35 40 45

Ala Ala Gly Leu Asp Leu Phe Gln Gly Asp Ile Leu Leu Gln Lys Ser  
 50 55 60

Arg Asn Gly Leu Arg Asp Pro Asn Thr Arg Trp Thr Phe Pro Ile Pro  
 65 70 75 80

Tyr Ile Leu Ala Asp Asn Leu Gly Leu Asn Ala Lys Gly Ala Ile Leu  
 85 90 95

Tyr Ala Phe Glu Met Phe Arg Leu Lys Ser Cys Val Asp Phe Lys Pro  
 100 105 110

Tyr Glu Gly Glu Ser Ser Tyr Ile Ile Phe Gln Gln Phe Asp Gly Cys  
 115 120 125

Trp Ser Glu Val Gly Asp Gln His Val Gly Gln Asn Ile Ser Ile Gly  
 130 135 140

Gln Gly Cys Ala Tyr Lys Ala Ile Ile Glu His Glu Ile Leu His Ala  
 145 150 155 160

Leu Gly Phe Tyr His Glu Gln Ser Arg Thr Asp Arg Asp Asp Tyr Val  
 165 170 175

Asn Ile Trp Trp Asp Gln Ile Leu Ser Gly Tyr Gln His Asn Phe Asp  
 180 185 190

Thr Tyr Asp Asp Ser Leu Ile Thr Asp Leu Asn Thr Pro Tyr Asp Tyr  
 195 200 205

Glu Ser Leu Met His Tyr Gln Pro Phe Ser Phe Asn Lys Asn Ala Ser  
 210 215 220

Val Pro Thr Ile Thr Ala Lys Ile Pro Glu Phe Asn Ser Ile Ile Gly  
 225 230 235 240

Gln Arg Leu Asp Phe Ser Ala Ile Asp Leu Glu Arg Leu Asn Arg Met  
245 250 255

Tyr Asn Cys Thr Thr Thr His Thr Leu Leu Asp His Cys Thr Phe Glu  
260 265 270

Lys Ala Asn Ile Cys Gly Met Ile Gln Gly Thr Arg Asp Asp Thr Asp  
275 280 285

Trp Ala His Gln Asp Ser Ala Gln Ala Gly Glu Val Asp His Thr Leu  
290 295 300

Leu Gly Gln Cys Thr Gly Ala Gly Tyr Phe Met Gln Phe Ser Thr Ser  
305 310 315 320

Ser Gly Ser Ala Glu Glu Ala Ala Leu Leu Glu Ser Arg Ile Leu Tyr  
325 330 335

Pro Lys Arg Lys Gln Gln Cys Leu Gln Phe Phe Tyr Lys Met Thr Gly  
340 345 350

Ser Pro Ser Asp Arg Leu Val Val Trp Val Arg Arg Asp Asp Ser Thr  
355 360 365

Gly Asn Val Arg Lys Leu Val Lys Val Gln Thr Phe Gln Gly Asp Asp  
370 375 380

Asp His Asn Trp Lys Ile Ala His Val Val Leu Lys Glu Glu Gln Lys  
385 390 395 400

Phe Arg Tyr Leu Phe Gln Gly Thr Lys Gly Asp Pro Gln Asn Ser Thr  
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Gly Gly Ile Tyr Leu Asp Asp Ile Thr Leu Thr Glu Thr Pro Cys Pro  
420 425 430

Thr Gly Val Trp Thr Val Arg Asn Phe Ser Gln Val Leu Glu Asn Thr  
435 440 445

Ser Lys Gly Asp Lys Leu Gln Ser Pro Arg Phe Tyr Asn Ser Glu Gly  
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Tyr Gly Phe Gly Val Thr Leu Tyr Pro Asn Ser Arg Glu Ser Ser Gly  
465 470 475 480

Tyr Leu Arg Leu Ala Phe His Val Cys Ser Gly Glu Asn Asp Ala Ile  
485 490 495

Leu Glu Trp Pro Val Glu Asn Arg Gln Val Ile Ile Thr Ile Leu Asp  
500 505 510

Gln Glu Pro Asp Val Arg Asn Arg Met Ser Ser Ser Met Val Phe Thr  
 515 520 525

Thr Ser Lys Ser His Thr Ser Pro Ala Ile Asn Asp Thr Val Ile Trp  
 530 535 540

Asp Arg Pro Ser Arg Val Gly Thr Tyr His Thr Asp Cys Asn Cys Phe  
 545 550 555 560

Arg Ser Ile Asp Leu Gly Trp Ser Gly Phe Ile Ser His Gln Met Leu  
 565 570 575

Lys Arg Arg Ser Phe Leu Lys Asn Asp Asp Leu Ile Ile Phe Val Asp  
 580 585 590

Phe Glu Asp Ile Thr His Leu Ser Gln Thr Glu Val Pro Ser Lys Gly  
 595 600 605

Lys Arg Leu Ser Pro Gln Gly Leu Ile Leu Gln Gly Gln Glu Gln Gln  
 610 615 620

Val Ser Glu Glu Gly Ser Gly Lys Ala Met Leu Glu Glu Ala Leu Pro  
 625 630 635 640

Val Ser Leu Ser Gln Gly Gln Pro Ser Arg Gln Lys Arg Ser Val Glu  
 645 650 655

Asn Thr Gly Pro Leu Glu Asp His Asn Trp Pro Gln Tyr Phe Arg Asp  
 660 665 670

Pro Cys Asp Pro Asn Pro Cys Gln Asn Asp Gly Ile Cys Val Asn Val  
 675 680 685

Lys Gly Met Ala Ser Cys Arg Cys Ile Ser Gly His Ala Phe Phe Tyr  
 690 695 700

Thr Gly Glu Arg Cys Gln Ser Ala Glu Val His Gly Ser Val Leu Gly  
 705 710 715 720

Met Val Ile Gly Gly Thr Ala Gly Val Ile Phe Leu Thr Phe Ser Ile  
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Ile Ala Ile Leu Ser Gln Arg Pro Arg Lys  
 740 745

<210> 63

<211> 8838

<212> DNA

<213> NM\_015902 EDD, hyperplastic discs protein, DD5

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (34)..(8430)

&lt;223&gt;

&lt;400&gt; 63

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                   1                   5

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Val His Pro Leu Pro Gly Thr Glu Asp Gln Leu Asn Asp Arg Leu Arg
      10                   15                   20

gaa gtt tct gag aag ctg aac aaa tat aat tta aac agc cac ccc cct      150
Glu Val Ser Glu Lys Leu Asn Lys Tyr Asn Leu Asn Ser His Pro Pro
      25                   30                   35

ttg aat gta ttg gaa cag gct act att aaa cag tgt gtg gtg gga cca      198
Leu Asn Val Leu Glu Gln Ala Thr Ile Lys Gln Cys Val Val Gly Pro
      40                   45                   50                   55

aat cat gct gcc ttt ctt ctt gag gat ggt aga gtt tgc agg att ggt      246
Asn His Ala Ala Phe Leu Leu Glu Asp Gly Arg Val Cys Arg Ile Gly
                   60                   65                   70

ttt tca gta cag cca gac aga ttg gaa ttg ggt aaa cct gat aat aat      294
Phe Ser Val Gln Pro Asp Arg Leu Glu Leu Gly Lys Pro Asp Asn Asn
                   75                   80                   85

gat ggg tca aag ttg aac agc aac tgc ggg gca ggg agg acg tca agg      342
Asp Gly Ser Lys Leu Asn Ser Asn Ser Gly Ala Gly Arg Thr Ser Arg
      90                   95                   100

cct ggt agg aca agc gac tct cca tgg ttt ctc tca ggt tct gag act      390
Pro Gly Arg Thr Ser Asp Ser Pro Trp Phe Leu Ser Gly Ser Glu Thr
      105                   110                   115

cta ggc agg ctg gca ggc aac acc tta gga agc cgc tgg agt tct gga      438
Leu Gly Arg Leu Ala Gly Asn Thr Leu Gly Ser Arg Trp Ser Ser Gly
      120                   125                   130                   135

gtg ggt gga agt ggt gga gga tcc tct ggt agg tca tca gct gga gct      486
Val Gly Gly Ser Gly Gly Gly Ser Ser Gly Arg Ser Ser Ala Gly Ala
      140                   145                   150

cga gat tcc cgc cgg cag act cga gtt att cgg aca gga cgg gat cga      534
Arg Asp Ser Arg Arg Gln Thr Arg Val Ile Arg Thr Gly Arg Asp Arg
      155                   160                   165

ggg tct ggg ctt ttg ggc agt cag ccc cag cca gtt att cca gca tct      582
Gly Ser Gly Leu Leu Gly Ser Gln Pro Gln Pro Val Ile Pro Ala Ser
      170                   175                   180

gtc att cca gag gag ctg att tca cag gcc caa gtt gtt tta caa ggc      630
Val Ile Pro Glu Glu Leu Ile Ser Gln Ala Gln Val Val Leu Gln Gly
      185                   190                   195

aaa tcc aga agt gtc att att cga gaa ctt cag aga aca aat ctt gat      678
Lys Ser Arg Ser Val Ile Ile Arg Glu Leu Gln Arg Thr Asn Leu Asp
      200                   205                   210                   215

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gtg aac ctt gct gta aat aat tta ctt agc cgg gat gat gaa gat gga Val Asn Leu Ala Val Asn Asn Leu Leu Ser Arg Asp Asp Glu Asp Gly 220 225 230	726
gat gat ggg gat gat aca gcc agc gaa tct tat ttg cct gga gag gat Asp Asp Gly Asp Asp Thr Ala Ser Glu Ser Tyr Leu Pro Gly Glu Asp 235 240 245	774
ctt atg tct ctc ctt gat gcc gac att cat tct gcc cac cca agt gtc Leu Met Ser Leu Leu Asp Ala Asp Ile His Ser Ala His Pro Ser Val 250 255 260	822
att att gat gca gat gcc atg ttt tct gaa gac att agc tat ttt ggt Ile Ile Asp Ala Asp Ala Met Phe Ser Glu Asp Ile Ser Tyr Phe Gly 265 270 275	870
tac cct tct ttt cgt cgt tca tca ctt tcc agg cta ggc tca tct cga Tyr Pro Ser Phe Arg Arg Ser Ser Leu Ser Arg Leu Gly Ser Ser Arg 280 285 290 295	918
gtt ctc ctt ctt ccc tta gag aga gac tct gag ctg ttg cgt gaa cgt Val Leu Leu Leu Pro Leu Glu Arg Asp Ser Glu Leu Leu Arg Glu Arg 300 305 310	966
gaa tcc gtt tta cgt tta cgt gaa cga agg tgg ctt gat gga gcc tca Glu Ser Val Leu Arg Leu Arg Glu Arg Arg Trp Leu Asp Gly Ala Ser 315 320 325	1014
ttt gat aat gaa agg ggt tct acc agc aag gaa gga gag cca aac ttg Phe Asp Asn Glu Arg Gly Ser Thr Ser Lys Glu Gly Glu Pro Asn Leu 330 335 340	1062
gat aag aag aat aca cct gtt caa agt cca gta tct cta gga gaa gat Asp Lys Lys Asn Thr Pro Val Gln Ser Pro Val Ser Leu Gly Glu Asp 345 350 355	1110
ttg cag tgg tgg cct gat aag gat gga aca aaa ttc atc tgt att ggg Leu Gln Trp Trp Pro Asp Lys Asp Gly Thr Lys Phe Ile Cys Ile Gly 360 365 370 375	1158
gct ctg tat tct gaa ctt ctg gct gtc agc agt aaa gga gaa ctt tat Ala Leu Tyr Ser Glu Leu Leu Ala Val Ser Ser Lys Gly Glu Leu Tyr 380 385 390	1206
cag tgg aaa tgg agt gaa tct gag cct tac aga aat gcc cag aat cct Gln Trp Lys Trp Ser Glu Ser Glu Pro Tyr Arg Asn Ala Gln Asn Pro 395 400 405	1254
tca tta cat cat cca cga gca aca ttt ttg ggg tta acc aat gaa aag Ser Leu His His Pro Arg Ala Thr Phe Leu Gly Leu Thr Asn Glu Lys 410 415 420	1302
ata gtc ctc ctg tct gca aat agc ata aga gca act gta gct aca gaa Ile Val Leu Leu Ser Ala Asn Ser Ile Arg Ala Thr Val Ala Thr Glu 425 430 435	1350
aat aac aag gtt gct aca tgg gtg gat gaa act tta agt tct gtg gct Asn Asn Lys Val Ala Thr Trp Val Asp Glu Thr Leu Ser Ser Val Ala 440 445 450 455	1398
tct aaa tta gag cac act gct cag act tac tct gaa ctt caa gga gag Ser Lys Leu Glu His Thr Ala Gln Thr Tyr Ser Glu Leu Gln Gly Glu 460 465 470	1446
cgg ata gtt tct tta cat tgc tgt gcc ctt tac acc tgc gct cag ctg Arg Ile Val Ser Leu His Cys Cys Ala Leu Tyr Thr Cys Ala Gln Leu 475 480 485	1494

gaa aac agt tta tat tgg tgg ggt gta gtt cct ttt agt caa agg aag Glu Asn Ser Leu Tyr Trp Trp Gly Val Val Pro Phe Ser Gln Arg Lys 490 495 500	1542
aaa atg tta gag aaa gct aga gca aaa aat aaa aag cct aaa tcc agt Lys Met Leu Glu Lys Ala Arg Ala Lys Asn Lys Lys Pro Lys Ser Ser 505 510 515	1590
gct ggt att tct tca atg ccg aac atc act gtt ggt acc cag gta tgc Ala Gly Ile Ser Ser Met Pro Asn Ile Thr Val Gly Thr Gln Val Cys 520 525 530 535	1638
ttg aga aat aat cct ctt tat cat gct gga gca gtt gca ttt tca att Leu Arg Asn Asn Pro Leu Tyr His Ala Gly Ala Val Ala Phe Ser Ile 540 545 550	1686
agt gct ggg att cct aaa gtt ggt gtc tta atg gag tca gtt tgg aat Ser Ala Gly Ile Pro Lys Val Gly Val Leu Met Glu Ser Val Trp Asn 555 560 565	1734
atg aat gac agc tgt aga ttt caa ctt aga tct cct gaa agc ttg aaa Met Asn Asp Ser Cys Arg Phe Gln Leu Arg Ser Pro Glu Ser Leu Lys 570 575 580	1782
aac atg gaa aaa gct agc aaa act act gaa gct aag cct gaa agt aag Asn Met Glu Lys Ala Ser Lys Thr Thr Glu Ala Lys Pro Glu Ser Lys 585 590 595	1830
cag gag cca gtg aaa aca gaa atg ggt cct cca cca tct cca gca tcc Gln Glu Pro Val Lys Thr Glu Met Gly Pro Pro Pro Ser Pro Ala Ser 600 605 610 615	1878
acg tgt agt gat gca tcc tca att gcc agc agt gca tca atg cca tac Thr Cys Ser Asp Ala Ser Ser Ile Ala Ser Ser Ala Ser Met Pro Tyr 620 625 630	1926
aaa cga cga cgg tca acc cct gca cca aaa gaa gag gaa aag gtg aat Lys Arg Arg Arg Ser Thr Pro Ala Pro Lys Glu Glu Glu Lys Val Asn 635 640 645	1974
gaa gag cag tgg tct ctt cgg gaa gtg gtt ttt gtg gaa gat gtc aag Glu Glu Gln Trp Ser Leu Arg Glu Val Val Phe Val Glu Asp Val Lys 650 655 660	2022
aat gtt cct gtt ggc aag gtg cta aaa gta gat ggt gcc tat gtt gct Asn Val Pro Val Gly Lys Val Leu Lys Val Asp Gly Ala Tyr Val Ala 665 670 675	2070
gta aaa ttt cca gga acc tcc agt aat act aac tgt cag aac agc tct Val Lys Phe Pro Gly Thr Ser Ser Asn Thr Asn Cys Gln Asn Ser Ser 680 685 690 695	2118
ggt cca gat gct gac cct tct tct ctc ctg cag gat tgt agg tta ctt Gly Pro Asp Ala Asp Pro Ser Ser Leu Leu Gln Asp Cys Arg Leu Leu 700 705 710	2166
aga att gat gaa ttg cag gtt gtc aaa act ggt gga aca ccg aag gtt Arg Ile Asp Glu Leu Gln Val Val Lys Thr Gly Gly Thr Pro Lys Val 715 720 725	2214
ccc gac tgt ttc caa agg act cct aaa aag ctt tgt ata cct gaa aaa Pro Asp Cys Phe Gln Arg Thr Pro Lys Lys Leu Cys Ile Pro Glu Lys 730 735 740	2262
aca gaa ata tta gca gtg aat gta gat tcc aaa ggt gtt cat gct gtt Thr Glu Ile Leu Ala Val Asn Val Asp Ser Lys Gly Val His Ala Val 745 750 755	2310

ctg aag act gga aat tgg gtg cga tac tgt atc ttt gat ctt gct aca Leu Lys Thr Gly Asn Trp Val Arg Tyr Cys Ile Phe Asp Leu Ala Thr 760 765 770 775	2358
gga aaa gca gaa cag gaa aat aat ttt cct aca agc agc att gct ttc Gly Lys Ala Glu Gln Glu Asn Asn Phe Pro Thr Ser Ser Ile Ala Phe 780 785 790	2406
ctt ggt cag aat gag agg aat gta gcc att ttc act gct gga cag gaa Leu Gly Gln Asn Glu Arg Asn Val Ala Ile Phe Thr Ala Gly Gln Glu 795 800 805	2454
tct ccc att att ctt cga gat gga aat ggt acc atc tac cca atg gcc Ser Pro Ile Ile Leu Arg Asp Gly Asn Gly Thr Ile Tyr Pro Met Ala 810 815 820	2502
aaa gat tgc atg gga gga ata agg gat ccc gat tgg ctg gat ctt cca Lys Asp Cys Met Gly Gly Ile Arg Asp Pro Asp Trp Leu Asp Leu Pro 825 830 835	2550
cct att agt agt ctt gga atg ggt gtg cat tct tta ata aat ctt cct Pro Ile Ser Ser Leu Gly Met Gly Val His Ser Leu Ile Asn Leu Pro 840 845 850 855	2598
gcc aat tca aca atc aaa aag aaa gct gct gtt atc atc atg gct gta Ala Asn Ser Thr Ile Lys Lys Lys Ala Ala Val Ile Ile Met Ala Val 860 865 870	2646
gag aaa caa acc tta atg caa cac att ctg cgc tgt gac tat gag gcc Glu Lys Gln Thr Leu Met Gln His Ile Leu Arg Cys Asp Tyr Glu Ala 875 880 885	2694
tgt cga caa tat cta atg aat ctt gag caa gcg gtt gtt tta gag cag Cys Arg Gln Tyr Leu Met Asn Leu Glu Gln Ala Val Val Leu Glu Gln 890 895 900	2742
aat cta cag atg ctg cag aca ttc atc agc cac aga tgt gat gga aat Asn Leu Gln Met Leu Gln Thr Phe Ile Ser His Arg Cys Asp Gly Asn 905 910 915	2790
cga aat att ttg cat gct tgt gta tca gtt tgc ttt cca acc agc aat Arg Asn Ile Leu His Ala Cys Val Ser Val Cys Phe Pro Thr Ser Asn 920 925 930 935	2838
aaa gaa act aaa gaa gaa gag gaa gcg gag cgt tct gaa aga aat aca Lys Glu Thr Lys Glu Glu Glu Ala Glu Arg Ser Glu Arg Asn Thr 940 945 950	2886
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gtt gtt tca agt aat ggc cca ggt aat cgg gct gga tca tca agt agc Val Val Ser Ser Asn Gly Pro Gly Asn Arg Ala Gly Ser Ser Ser Ser 970 975 980	2982
cga agt ttg aga tta cgg gaa atg atg aga cgt tcg ttg aga gca gct Arg Ser Leu Arg Leu Arg Glu Met Met Arg Arg Ser Leu Arg Ala Ala 985 990 995	3030
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gat cca gtt tca ccc ccc ata gct ccc cct agt tgg gtt cct gac Asp Pro Val Ser Pro Pro Ile Ala Pro Pro Ser Trp Val Pro Asp 1015 1020 1025	3120

cct Pro 1030	cct Pro 1030	gcg Ala 1030	atg Met 1030	gat Asp 1030	cct Pro 1035	gat Asp 1035	ggg Gly 1035	gac Asp 1035	att Ile 1035	gat Asp 1040	ttt Phe 1040	atc Ile 1040	ctg Leu 1040	gcc Ala 1040	3165
ccc Pro 1045	gct Ala 1045	gtg Val 1045	gga Gly 1045	tct Ser 1045	ctt Leu 1050	acc Thr 1050	aca Thr 1050	gca Ala 1050	gca Ala 1050	acc Thr 1055	ggg Gly 1055	act Thr 1055	ggg Gly 1055	caa Gln 1055	3210
gga Gly 1060	cca Pro 1060	agc Ser 1060	acc Thr 1060	tcc Ser 1060	act Thr 1065	att Ile 1065	cca Pro 1065	ggg Gly 1065	cct Pro 1070	tcc Ser 1070	aca Thr 1070	gag Glu 1070	cca Pro 1070	tct Ser 1070	3255
gta Val 1075	gta Val 1075	gaa Glu 1075	tcc Ser 1075	aag Lys 1075	gat Asp 1080	cga Arg 1080	aag Lys 1080	gcg Ala 1080	aat Asn 1080	gct Ala 1085	cat His 1085	ttt Phe 1085	ata Ile 1085	ttg Leu 1085	3300
aaa Lys 1090	ttg Leu 1090	tta Leu 1090	tgt Cys 1090	gac Asp 1090	agt Ser 1095	gtg Val 1095	gtt Val 1095	ctc Leu 1095	cag Gln 1095	ccc Pro 1100	tat Tyr 1100	cta Leu 1100	cga Arg 1100	gaa Glu 1100	3345
ctt Leu 1105	ctt Leu 1105	tct Ser 1105	gcc Ala 1105	aag Lys 1105	gat Asp 1110	gca Ala 1110	aga Arg 1110	ggg Gly 1110	atg Met 1110	acc Thr 1115	cca Pro 1115	ttt Phe 1115	atg Met 1115	tca Ser 1115	3390
gct Ala 1120	gta Val 1120	agt Ser 1120	ggc Gly 1120	cga Arg 1120	gct Ala 1125	tat Tyr 1125	cct Pro 1125	gct Ala 1125	gca Ala 1125	att Ile 1130	acc Thr 1130	atc Ile 1130	tta Leu 1130	gaa Glu 1130	3435
act Thr 1135	gct Ala 1135	cag Gln 1135	aaa Lys 1135	att Ile 1135	gca Ala 1140	aaa Lys 1140	gct Ala 1140	gaa Glu 1140	ata Ile 1140	tcc Ser 1145	tca Ser 1145	agt Ser 1145	gaa Glu 1145	aaa Lys 1145	3480
gag Glu 1150	gaa Glu 1150	gat Asp 1150	gta Val 1150	ttc Phe 1150	atg Met 1155	gga Gly 1155	atg Met 1155	gtt Val 1155	tgc Cys 1155	cca Pro 1160	tca Ser 1160	ggg Gly 1160	acc Thr 1160	aac Asn 1160	3525
cct Pro 1165	gat Asp 1165	gac Asp 1165	tct Ser 1165	cct Pro 1165	tta Leu 1170	tat Tyr 1170	gtt Val 1170	tta Leu 1170	tgt Cys 1170	tgt Cys 1175	aat Asn 1175	gac Asp 1175	act Thr 1175	tgc Cys 1175	3570
agt Ser 1180	ttt Phe 1180	aca Thr 1180	tgg Trp 1180	act Thr 1180	gga Gly 1185	gca Ala 1185	gag Glu 1185	cac His 1185	att Ile 1185	aac Asn 1190	cag Gln 1190	gat Asp 1190	att Ile 1190	ttt Phe 1190	3615
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gaa Glu 1210	tgt Cys 1210	gca Ala 1210	agg Arg 1210	gtt Val 1210	tgt Cys 1215	cat His 1215	aaa Lys 1215	ggg Gly 1215	cat His 1215	gat Asp 1220	tgc Cys 1220	aaa Lys 1220	ctc Leu 1220	aaa Lys 1220	3705
cgg Arg 1225	aca Thr 1225	tca Ser 1225	cca Pro 1225	aca Thr 1225	gcc Ala 1230	tac Tyr 1230	tgt Cys 1230	gat Asp 1230	tgt Cys 1230	tgg Trp 1235	gag Glu 1235	aaa Lys 1235	tgt Cys 1235	aaa Lys 1235	3750
tgt Cys 1240	aaa Lys 1240	act Thr 1240	ctt Leu 1240	att Ile 1240	gct Ala 1245	gga Gly 1245	cag Gln 1245	aaa Lys 1245	tct Ser 1245	gct Ala 1250	cgt Arg 1250	ctt Leu 1250	gat Asp 1250	cta Leu 1250	3795
ctt Leu 1255	tat Tyr 1255	cgc Arg 1255	ctg Leu 1255	ctc Leu 1255	act Thr 1260	gct Ala 1260	act Thr 1260	aat Asn 1260	ctg Leu 1260	gtt Val 1265	act Thr 1265	ctg Leu 1265	cca Pro 1265	aac Asn 1265	3840
agc Ser 1270	agg Arg 1270	gga Gly 1270	gag Glu 1270	cac His 1270	ctc Leu 1275	tta Leu 1275	cta Leu 1275	ttc Phe 1275	tta Leu 1275	gta Val 1280	cag Gln 1280	aca Thr 1280	gtc Val 1280	gca Ala 1280	3885



agg Arg 1285	cag Gln	acg Thr	gtg Val	gag Glu	cat His 1290	tgt Cys	caa Gln	tac Tyr	agg Arg	cca Pro 1295	cct Pro	cga Arg	atc Ile	agg Arg	3930
gaa Glu 1300	gat Asp	cgt Arg	aac Asn	cga Arg	aaa Lys 1305	aca Thr	gcc Ala	agt Ser	cct Pro	gaa Glu 1310	gat Asp	tca Ser	gat Asp	atg Met	3975
cca Pro 1315	gat Asp	cat His	gat Asp	tta Leu	gag Glu 1320	cct Pro	cca Pro	aga Arg	ttt Phe	gcc Ala 1325	cag Gln	ctt Leu	gca Ala	ttg Leu	4020
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cta Leu 1405	gtg Val	aaa Lys	gaa Glu	ctc Leu	caa Gln 1410	aac Asn	aaa Lys	tat Tyr	aca Thr	cct Pro 1415	gga Gly	cgt Arg	aga Arg	gaa Glu	4290
gaa Glu 1420	gct Ala	att Ile	gct Ala	gtg Val	aca Thr 1425	atg Met	agg Arg	ttt Phe	cta Leu	cgt Arg 1430	tca Ser	gtg Val	gca Ala	aga Arg	4335
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caa Gln 1465	gca Ala	ttg Leu	cta Leu	cct Pro	tac Tyr 1470	gct Ala	gtg Val	gaa Glu	gaa Glu	ttg Leu 1475	tgc Cys	aac Asn	gta Val	gca Ala	4470
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agt Ser 1510	gaa Glu	gaa Glu	tta Leu	ttt Phe	tca Ser 1515	gtg Val	gaa Glu	cca Pro	cta Leu	cca Pro 1520	cca Pro	cga Arg	cca Pro	tca Ser	4605
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cgg Arg 1555	ggc Gly	aga Arg	gat Asp	gaa Glu	gaa Glu 1560	cag Gln	gat Asp	gat Asp	att Ile	gtt Val 1565	tca Ser	gca Ala	gat Asp	gtg Val	4740
gaa Glu 1570	gag Glu	gtt Val	gag Glu	gtg Val	gtg Val 1575	gag Glu	ggg Gly	gtg Val	gct Ala	gga Gly 1580	gaa Glu	gag Glu	gat Asp	cat His	4785
cat His 1585	gat Asp	gaa Glu	cag Gln	gaa Glu	gaa Glu 1590	cac His	ggg Gly	gaa Glu	gaa Glu	aat Asn 1595	gct Ala	gag Glu	gca Ala	gag Glu	4830
gga Gly 1600	caa Gln	cat His	gat Asp	gag Glu	cat His 1605	gat Asp	gaa Glu	gac Asp	ggg Gly	agt Ser 1610	gat Asp	atg Met	gag Glu	ctg Leu	4875
gac Asp 1615	ttg Leu	tta Leu	gca Ala	gca Ala	gct Ala 1620	gaa Glu	aca Thr	gaa Glu	agt Ser	gat Asp 1625	agt Ser	gaa Glu	agt Ser	aac Asn	4920
cac His 1630	agc Ser	aac Asn	caa Gln	gat Asp	aat Asn 1635	gct Ala	agt Ser	ggg Gly	cgc Arg	aga Arg 1640	agc Ser	gtt Val	gtc Val	act Thr	4965
gca Ala 1645	gca Ala	act Thr	gct Ala	ggg Gly	tca Ser 1650	gaa Glu	gca Ala	gga Gly	gca Ala	agc Ser 1655	agt Ser	gtt Val	cct Pro	gcc Ala	5010
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atg Met 1690	ctt Leu	gat Asp	gag Glu	cca Pro	tta Leu 1695	gaa Glu	aga Arg	acc Thr	aca Thr	aat Asn 1700	agc Ser	tcc Ser	cat His	gcc Ala	5145
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tct Ser 1735	aca Thr	cca Pro	gca Ala	gca Ala	agt Ser 1740	tca Ser	gcg Ala	ggg Gly	ttg Leu	att Ile 1745	tat Tyr	att Ile	gat Asp	cct Pro	5280
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gca Ala 1765	gca Ala	gct Ala	gct Ala	ttg Leu	gaa Glu 1770	gct Ala	agc Ser	aac Asn	gcc Ala	agc Ser 1775	agt Ser	tac Tyr	cta Leu	aca Thr	5370
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tac Tyr 1810	tct Ser	cag Gln	att Ile	cca Pro	gca Ala 1815	gct Ala	gtg Val	aaa Lys	ttg Leu	act Thr 1820	tac Tyr	caa Gln	gat Asp	gca Ala	5505
gta Val 1825	aac Asn	tta Leu	cag Gln	aac Asn	tat Tyr 1830	gta Val	gaa Glu	gaa Glu	aag Lys	ctt Leu 1835	att Ile	ccc Pro	act Thr	tgg Trp	5550
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cat His 1870	cct Pro	ctt Leu	cac His	gct Ala	tct Ser 1875	cag Gln	aat Asn	tca Ser	gcg Ala	aga Arg 1880	aga Arg	gag Glu	agg Arg	atg Met	5685
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aag Lys 1945	cat His	gtg Val	gca Ala	tat Tyr	gtt Val 1950	ttt Phe	caa Gln	gca Ala	ctt Leu	ata Ile 1955	tac Tyr	tgg Trp	att Ile	aag Lys	5910
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aaa Lys 1975	agg Arg	acg Thr	cga Arg	gaa Glu	ctc Leu 1980	ttg Leu	gaa Glu	ctg Leu	ggc Gly	att Ile 1985	gat Asp	aat Asn	gaa Glu	gat Asp	6000
tca Ser 1990	gaa Glu	cat His	gaa Glu	aat Asn	gat Asp 1995	gat Asp	gac Asp	acc Thr	aat Asn	caa Gln 2000	agt Ser	gct Ala	act Thr	ttg Leu	6045
aat Asn 2005	gat Asp	aag Lys	gat Asp	gat Asp	gac Asp 2010	tct Ser	ctt Leu	cct Pro	gca Ala	gaa Glu 2015	act Thr	ggc Gly	caa Gln	aac Asn	6090
cat His 2020	cca Pro	ttt Phe	ttc Phe	cga Arg	cgt Arg 2025	tca Ser	gac Asp	tcc Ser	atg Met	aca Thr 2030	ttc Phe	ctt Leu	ggg Gly	tgt Cys	6135
ata Ile 2035	ccc Pro	cca Pro	aat Asn	cca Pro	ttt Phe 2040	gaa Glu	gtg Val	cct Pro	ctg Leu	gct Ala 2045	gaa Glu	gcc Ala	atc Ile	ccc Pro	6180

ttg gct gat cag cca cat ctg ttg cag cca aat gct aga aag gag Leu Ala Asp Gln Pro His Leu Leu Gln Pro Asn Ala Arg Lys Glu 2050 2055 2060	6225
gat ctt ttt ggc cgt cca agt cag ggt ctt tat tct tca tct gcc Asp Leu Phe Gly Arg Pro Ser Gln Gly Leu Tyr Ser Ser Ser Ala 2065 2070 2075	6270
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tct gct cat gat ctt gct gca caa tta aaa agt agc tta cta gca Ser Ala His Asp Leu Ala Ala Gln Leu Lys Ser Ser Leu Leu Ala 2140 2145 2150	6495
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gat cgg gat cga gat ctt ctc att cag cag act atg agg cag ctt Asp Arg Asp Arg Asp Leu Leu Ile Gln Gln Thr Met Arg Gln Leu 2245 2250 2255	6810
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aga Arg 2365	aga cag ctt tcc atc Arg Gln Leu Ser Ile 2370	gac act agg ccc ttt Asp Thr Arg Pro Phe 2375	aga cca gcc tct Arg Pro Ala Ser	7170
gaa Glu 2380	ggg aat cct agc gat Gly Asn Pro Ser Asp 2385	gat cct gag cct ttg Asp Pro Glu Pro Leu 2390	cca gca cat cgg Pro Ala His Arg	7215
cag Gln 2395	gca ctt gga gag agg Ala Leu Gly Glu Arg 2400	ctt tat cct cgt gta Leu Tyr Pro Arg Val 2405	caa gca atg caa Gln Ala Met Gln	7260
cca Pro 2410	gca ttt gca agt aaa Ala Phe Ala Ser Lys 2415	atc act ggc atg ttg Ile Thr Gly Met Leu 2420	ttg gaa tta tcc Leu Glu Leu Ser	7305
cca Pro 2425	gct cag ctg ctt ctc Ala Gln Leu Leu Leu 2430	ctt cta gca agt gag Leu Leu Ala Ser Glu 2435	gat tct ctg aga Asp Ser Leu Arg	7350
gca Ala 2440	aga gtg gat gag gcc Arg Val Asp Glu Ala 2445	atg gaa ctc att att Met Glu Leu Ile Ile 2450	gca cat gga cgg Ala His Gly Arg	7395
gaa Glu 2455	aat gga gct gat agt Asn Gly Ala Asp Ser 2460	atc ctg gat ctt gga Ile Leu Asp Leu Gly 2465	tta gta gac tcc Leu Val Asp Ser	7440
tca Ser 2470	gaa aag gta cag cag Glu Lys Val Gln Gln 2475	gaa aac cga aag cgc Glu Asn Arg Lys Arg 2480	cat ggc tct agt His Gly Ser Ser	7485
cga Arg 2485	agt gta gta gat atg Ser Val Val Asp Met 2490	gat tta gat gat aca Asp Leu Asp Asp Thr 2495	gat gat ggt gat Asp Asp Gly Asp	7530
gac Asp 2500	aat gcc cct ttg ttt Asn Ala Pro Leu Phe 2505	tac caa cct ggg aaa Tyr Gln Pro Gly Lys 2510	aga gga ttt tat Arg Gly Phe Tyr	7575
act Thr 2515	cca agg cct ggc aag Pro Arg Pro Gly Lys 2520	aac aca gaa gca agg Asn Thr Glu Ala Arg 2525	ttg aat tgt ttc Leu Asn Cys Phe	7620
aga Arg 2530	aac att ggc agg att Asn Ile Gly Arg Ile 2535	ctt gga cta tgt ctg Leu Gly Leu Cys Leu 2540	tta cag aat gaa Leu Gln Asn Glu	7665
ctc Leu 2545	tgt cct atc aca ttg Cys Pro Ile Thr Leu 2550	aat aga cat gta att Asn Arg His Val Ile 2555	aaa gta ttg ctt Lys Val Leu Leu	7710



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<213> NM\_015902 EDD, hyperplastic discs protein, DD5

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Lys Gln Cys Val Val Gly Pro Asn His Ala Ala Phe Leu Leu Glu Asp  
50 55 60

Gly Arg Val Cys Arg Ile Gly Phe Ser Val Gln Pro Asp Arg Leu Glu  
65 70 75 80

Leu Gly Lys Pro Asp Asn Asn Asp Gly Ser Lys Leu Asn Ser Asn Ser  
85 90 95

Gly Ala Gly Arg Thr Ser Arg Pro Gly Arg Thr Ser Asp Ser Pro Trp  
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Phe Leu Ser Gly Ser Glu Thr Leu Gly Arg Leu Ala Gly Asn Thr Leu  
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Gly Ser Arg Trp Ser Ser Gly Val Gly Gly Ser Gly Gly Gly Ser Ser  
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Gly Arg Ser Ser Ala Gly Ala Arg Asp Ser Arg Arg Gln Thr Arg Val  
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Ile Arg Thr Gly Arg Asp Arg Gly Ser Gly Leu Leu Gly Ser Gln Pro  
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Gln Pro Val Ile Pro Ala Ser Val Ile Pro Glu Glu Leu Ile Ser Gln  
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Ala Gln Val Val Leu Gln Gly Lys Ser Arg Ser Val Ile Ile Arg Glu  
195 200 205

Leu Gln Arg Thr Asn Leu Asp Val Asn Leu Ala Val Asn Asn Leu Leu  
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Ser Arg Asp Asp Glu Asp Gly Asp Asp Gly Asp Asp Thr Ala Ser Glu  
225 230 235 240

Ser Tyr Leu Pro Gly Glu Asp Leu Met Ser Leu Leu Asp Ala Asp Ile  
245 250 255

His Ser Ala His Pro Ser Val Ile Ile Asp Ala Asp Ala Met Phe Ser  
260 265 270

Glu Asp Ile Ser Tyr Phe Gly Tyr Pro Ser Phe Arg Arg Ser Ser Leu  
275 280 285

Ser Arg Leu Gly Ser Ser Arg Val Leu Leu Leu Pro Leu Glu Arg Asp  
290 295 300

Ser Glu Leu Leu Arg Glu Arg Glu Ser Val Leu Arg Leu Arg Glu Arg  
305 310 315 320

Arg Trp Leu Asp Gly Ala Ser Phe Asp Asn Glu Arg Gly Ser Thr Ser  
325 330 335

Lys Glu Gly Glu Pro Asn Leu Asp Lys Lys Asn Thr Pro Val Gln Ser  
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Pro Val Ser Leu Gly Glu Asp Leu Gln Trp Trp Pro Asp Lys Asp Gly  
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Thr Lys Phe Ile Cys Ile Gly Ala Leu Tyr Ser Glu Leu Leu Ala Val  
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Ser Ser Lys Gly Glu Leu Tyr Gln Trp Lys Trp Ser Glu Ser Glu Pro  
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Tyr Arg Asn Ala Gln Asn Pro Ser Leu His His Pro Arg Ala Thr Phe  
405 410 415

Leu Gly Leu Thr Asn Glu Lys Ile Val Leu Leu Ser Ala Asn Ser Ile  
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Arg Ala Thr Val Ala Thr Glu Asn Asn Lys Val Ala Thr Trp Val Asp  
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Glu Thr Leu Ser Ser Val Ala Ser Lys Leu Glu His Thr Ala Gln Thr  
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Tyr Ser Glu Leu Gln Gly Glu Arg Ile Val Ser Leu His Cys Cys Ala  
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Leu Tyr Thr Cys Ala Gln Leu Glu Asn Ser Leu Tyr Trp Trp Gly Val  
485 490 495

Val Pro Phe Ser Gln Arg Lys Lys Met Leu Glu Lys Ala Arg Ala Lys  
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Asn Lys Lys Pro Lys Ser Ser Ala Gly Ile Ser Ser Met Pro Asn Ile  
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Thr Val Gly Thr Gln Val Cys Leu Arg Asn Asn Pro Leu Tyr His Ala  
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Gly Ala Val Ala Phe Ser Ile Ser Ala Gly Ile Pro Lys Val Gly Val  
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Val Phe Val Glu Asp Val Lys Asn Val Pro Val Gly Lys Val Leu Lys  
660 665 670

Val Asp Gly Ala Tyr Val Ala Val Lys Phe Pro Gly Thr Ser Ser Asn  
675 680 685

Thr Asn Cys Gln Asn Ser Ser Gly Pro Asp Ala Asp Pro Ser Ser Leu  
690 695 700

Leu Gln Asp Cys Arg Leu Leu Arg Ile Asp Glu Leu Gln Val Val Lys  
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Thr Gly Gly Thr Pro Lys Val Pro Asp Cys Phe Gln Arg Thr Pro Lys  
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Lys Leu Cys Ile Pro Glu Lys Thr Glu Ile Leu Ala Val Asn Val Asp  
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Ser Lys Gly Val His Ala Val Leu Lys Thr Gly Asn Trp Val Arg Tyr  
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Pro Thr Ser Ser Ile Ala Phe Leu Gly Gln Asn Glu Arg Asn Val Ala  
785 790 795 800

Ile Phe Thr Ala Gly Gln Glu Ser Pro Ile Ile Leu Arg Asp Gly Asn  
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820 825 830

Pro Asp Trp Leu Asp Leu Pro Pro Ile Ser Ser Leu Gly Met Gly Val  
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His Ser Leu Ile Asn Leu Pro Ala Asn Ser Thr Ile Lys Lys Lys Ala  
850 855 860

Ala Val Ile Ile Met Ala Val Glu Lys Gln Thr Leu Met Gln His Ile  
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Leu Arg Cys Asp Tyr Glu Ala Cys Arg Gln Tyr Leu Met Asn Leu Glu  
885 890 895

Gln Ala Val Val Leu Glu Gln Asn Leu Gln Met Leu Gln Thr Phe Ile  
900 905 910

Ser His Arg Cys Asp Gly Asn Arg Asn Ile Leu His Ala Cys Val Ser  
915 920 925

Val Cys Phe Pro Thr Ser Asn Lys Glu Thr Lys Glu Glu Glu Ala  
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Glu Arg Ser Glu Arg Asn Thr Phe Ala Glu Arg Leu Ser Ala Val Glu  
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Ala Ile Ala Asn Ala Ile Ser Val Val Ser Ser Asn Gly Pro Gly Asn  
965 970 975

Arg Ala Gly Ser Ser Ser Arg Ser Leu Arg Leu Arg Glu Met Met  
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Arg Arg Ser Leu Arg Ala Ala Gly Leu Gly Arg His Glu Ala Gly Ala  
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Ile Asp Phe Ile Leu Ala Pro Ala Val Gly Ser Leu Thr Thr Ala  
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Leu Val 1280	Gln Thr Val Ala Arg 1285	Gln Thr Val Glu His Cys Gln Tyr 1290
Arg Pro 1295	Pro Arg Ile Arg Glu 1300	Asp Arg Asn Arg Lys Thr Ala Ser 1305
Pro Glu 1310	Asp Ser Asp Met Pro 1315	Asp His Asp Leu Glu Pro Pro Arg 1320
Phe Ala 1325	Gln Leu Ala Leu Glu 1330	Arg Val Leu Gln Asp Trp Asn Ala 1335
Leu Lys 1340	Ser Met Ile Met Phe 1345	Gly Ser Gln Glu Asn Lys Asp Pro 1350
Leu Ser 1355	Ala Ser Ser Arg Ile 1360	Gly His Leu Leu Pro Glu Glu Gln 1365
Val Tyr 1370	Leu Asn Gln Gln Ser 1375	Gly Thr Ile Arg Leu Asp Cys Phe 1380
Thr His 1385	Cys Leu Ile Val Lys 1390	Cys Thr Ala Asp Ile Leu Leu Leu 1395
Asp Thr 1400	Leu Leu Gly Thr Leu 1405	Val Lys Glu Leu Gln Asn Lys Tyr 1410
Thr Pro 1415	Gly Arg Arg Glu Glu 1420	Ala Ile Ala Val Thr Met Arg Phe 1425
Leu Arg 1430	Ser Val Ala Arg Val 1435	Phe Val Ile Leu Ser Val Glu Met 1440
Ala Ser 1445	Ser Lys Lys Lys Asn 1450	Asn Phe Ile Pro Gln Pro Ile Gly 1455
Lys Cys 1460	Lys Arg Val Phe Gln 1465	Ala Leu Leu Pro Tyr Ala Val Glu 1470
Glu Leu 1475	Cys Asn Val Ala Glu 1480	Ser Leu Ile Val Pro Val Arg Met 1485

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 1910 1915 1920  
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Pro 2060	Asn	Ala	Arg	Lys	Glu	Asp 2065	Leu	Phe	Gly	Arg	Pro 2070	Ser	Gln	Gly
Leu 2075	Tyr	Ser	Ser	Ser	Ala	Ser 2080	Ser	Gly	Lys	Cys	Leu 2085	Met	Glu	Val
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 2495 2500 2505



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Cys Leu Leu Gln Asn Glu Leu Cys Pro Ile Thr Leu Asn Arg His  
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Val Ile Lys Val Leu Leu Gly Arg Lys Val Asn Trp His Asp Phe  
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Met Leu Ile Ser Phe Thr Ser Phe Asn Asp Glu Ser Gly Glu Asn  
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2720 2725 2730

Thr Ser Ser Pro Ser Leu Pro Ala Ser Glu Glu Gly Phe Gln Pro  
2735 2740 2745

Met Pro Ser Ile Thr Ile Arg Pro Pro Asp Asp Gln His Leu Pro  
2750 2755 2760

Thr Ala Asn Thr Cys Ile Ser Arg Leu Tyr Val Pro Leu Tyr Ser  
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cagcc atg gcc cca aga aag aga ggt gga cga ggt att tca ttc atc ttt 170  
Met Ala Pro Arg Lys Arg Gly Gly Arg Gly Ile Ser Phe Ile Phe  
1 5 10 15

tgc tgt ttc cga aat aat gat cac cca gaa atc acg tat cgg ctg cga 218  
Cys Cys Phe Arg Asn Asn Asp His Pro Glu Ile Thr Tyr Arg Leu Arg  
20 25 30

aat gat agc aac ttt gcg ctt cag acc atg gaa cca gca ttg ccc atg 266  
Asn Asp Ser Asn Phe Ala Leu Gln Thr Met Glu Pro Ala Leu Pro Met  
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ccc cct gtg gag gag ctg gat gtc atg ttc agt gaa ctg gtg gat gaa 314  
Pro Pro Val Glu Glu Leu Asp Val Met Phe Ser Glu Leu Val Asp Glu  
50 55 60

ctg gac ctc aca gac aaa cac aga gaa gcc atg ttt gca ctt cca gct 362  
Leu Asp Leu Thr Asp Lys His Arg Glu Ala Met Phe Ala Leu Pro Ala  
65 70 75

gag aaa aaa tgg caa ata tac tgt agc aag aaa aag gac cag gaa gaa 410  
Glu Lys Lys Trp Gln Ile Tyr Cys Ser Lys Lys Lys Asp Gln Glu Glu  
80 85 90 95

aac aag gga gct aca agt tgg cct gaa ttc tac att gat cag ctc aat 458  
Asn Lys Gly Ala Thr Ser Trp Pro Glu Phe Tyr Ile Asp Gln Leu Asn  
100 105 110

tcc atg gct gct aga aaa tct ctg ctg gct tta gag aag gaa gaa gaa 506  
Ser Met Ala Ala Arg Lys Ser Leu Leu Ala Leu Glu Lys Glu Glu Glu

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aaa cca atg agg ttt gta acc aga ttc atc gac ttg gat ggc cta tca Lys Pro Met Arg Phe Val Thr Arg Phe Ile Asp Leu Asp Gly Leu Ser 145 150 155			602
tgt atc ctc aac ttt cta aag acc atg gac tac gag acc tca gag tct Cys Ile Leu Asn Phe Leu Lys Thr Met Asp Tyr Glu Thr Ser Glu Ser 160 165 170 175			650
cga ata cat act tct ctc att ggc tgt ata aag gcg tta atg aac aac Arg Ile His Thr Ser Leu Ile Gly Cys Ile Lys Ala Leu Met Asn Asn 180 185 190			698
tct caa ggc cgg gct cac gtc ctg gct cat tct gag agt att aat gta Ser Gln Gly Arg Ala His Val Leu Ala His Ser Glu Ser Ile Asn Val 195 200 205			746
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cgc ttt cag aca tta att aac gac ttg gat aaa agc act ggg cgg tat Arg Phe Gln Thr Leu Ile Asn Asp Leu Asp Lys Ser Thr Gly Arg Tyr 260 265 270			938
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att aag aat gtc gta cga atg ttg gtt aat gaa aat gaa gtt aag cag Ile Lys Asn Val Val Arg Met Leu Val Asn Glu Asn Glu Val Lys Gln 435 440 445			1466
tgg aaa gaa caa gcg gaa aaa atg aga aaa gag cac aat gag cta caa Trp Lys Glu Gln Ala Glu Lys Met Arg Lys Glu His Asn Glu Leu Gln 450 455 460			1514
cag aaa ctg gaa aag aaa gaa cga gaa tgt gat gct aag act caa gag Gln Lys Leu Glu Lys Lys Glu Arg Glu Cys Asp Ala Lys Thr Gln Glu 465 470 475			1562
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aag gag act act gag cat aag caa gtc aag cag cag gtg gcg gac ctc Lys Glu Thr Thr Glu His Lys Gln Val Lys Gln Gln Val Ala Asp Leu 500 505 510			1658
aca gca cag ctc cat gag ctc agc agg agg gcc gtc tgt gct tca atc Thr Ala Gln Leu His Glu Leu Ser Arg Arg Ala Val Cys Ala Ser Ile 515 520 525			1706
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cta gat ctt gaa gac ctg gaa aga acc ttc tct gcc tat caa aga cag Leu Asp Leu Glu Asp Leu Glu Arg Thr Phe Ser Ala Tyr Gln Arg Gln 640 645 650 655			2090
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aaa tta tcc aat gac gaa atc aaa cgg gca att cta aca atg gac gaa Lys Leu Ser Asn Asp Glu Ile Lys Arg Ala Ile Leu Thr Met Asp Glu 705 710 715			2282
cag gaa gat ctg ccc aag gac atg ttg gaa cag ctc ttg aaa ttt gtt Gln Glu Asp Leu Pro Lys Asp Met Leu Glu Gln Leu Leu Lys Phe Val 720 725 730 735			2330
cct gaa aaa agt gac att gac cta ttg gag gaa cat aaa cac gaa ctg Pro Glu Lys Ser Asp Ile Asp Leu Leu Glu Glu His Lys His Glu Leu 740 745 750			2378
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toc agc atc gac aaa aac att acc ctt ttg cac tat ctc atc act att Ser Ser Ile Asp Lys Asn Ile Thr Leu Leu His Tyr Leu Ile Thr Ile 850 855 860			2714
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gat att cct caa gct gcg aaa gta aac atg act gag ctg gac aaa gaa Asp Ile Pro Gln Ala Ala Lys Val Asn Met Thr Glu Leu Asp Lys Glu 880 885 890 895			2810
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930	935	940	
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tca gct tta cgc tca gga gaa gtg ttt gac aaa gac ctt tct aaa Ser Ala Leu Arg Ser Gly Glu Val Phe Asp Lys Asp Leu Ser Lys 1040 1045 1050			3281
ttg aaa cgg aat cgc aaa cgt att acc aac cag atg act gac agc Leu Lys Arg Asn Arg Lys Arg Ile Thr Asn Gln Met Thr Asp Ser 1055 1060 1065			3326
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&lt;400&gt; 66

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Asp Ser Asn Phe Ala Leu Gln Thr Met Glu Pro Ala Leu Pro Met Pro  
 35 40 45

Pro Val Glu Glu Leu Asp Val Met Phe Ser Glu Leu Val Asp Glu Leu  
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Asp Leu Thr Asp Lys His Arg Glu Ala Met Phe Ala Leu Pro Ala Glu  
 65 70 75 80

Lys Lys Trp Gln Ile Tyr Cys Ser Lys Lys Lys Asp Gln Glu Glu Asn  
 85 90 95

Lys Gly Ala Thr Ser Trp Pro Glu Phe Tyr Ile Asp Gln Leu Asn Ser  
 100 105 110

Met Ala Ala Arg Lys Ser Leu Leu Ala Leu Glu Lys Glu Glu Glu Glu  
 115 120 125

Glu Arg Ser Lys Thr Ile Glu Ser Leu Lys Thr Ala Leu Arg Thr Lys  
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Pro Met Arg Phe Val Thr Arg Phe Ile Asp Leu Asp Gly Leu Ser Cys  
 145 150 155 160

Ile Leu Asn Phe Leu Lys Thr Met Asp Tyr Glu Thr Ser Glu Ser Arg  
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Ile His Thr Ser Leu Ile Gly Cys Ile Lys Ala Leu Met Asn Asn Ser  
 180 185 190

Gln Gly Arg Ala His Val Leu Ala His Ser Glu Ser Ile Asn Val Ile  
 195 200 205

Ala Gln Ser Leu Ser Thr Glu Asn Ile Lys Thr Lys Val Ala Val Leu  
 210 215 220

Glu Ile Leu Gly Ala Val Cys Leu Val Pro Gly Gly His Lys Lys Val  
225 230 235 240

Leu Gln Ala Met Leu His Tyr Gln Lys Tyr Ala Ser Glu Arg Thr Arg  
245 250 255

Phe Gln Thr Leu Ile Asn Asp Leu Asp Lys Ser Thr Gly Arg Tyr Arg  
260 265 270

Asp Glu Val Ser Leu Lys Thr Ala Ile Met Ser Phe Ile Asn Ala Val  
275 280 285

Leu Ser Gln Gly Ala Gly Val Glu Ser Leu Asp Phe Arg Leu His Leu  
290 295 300

Arg Tyr Glu Phe Leu Met Leu Gly Ile Gln Pro Val Ile Asp Lys Leu  
305 310 315 320

Arg Glu His Glu Asn Ser Thr Leu Asp Arg His Leu Asp Phe Phe Glu  
325 330 335

Met Leu Arg Asn Glu Asp Glu Leu Glu Phe Ala Lys Arg Phe Glu Leu  
340 345 350

Val His Ile Asp Thr Lys Ser Ala Thr Gln Met Phe Glu Leu Thr Arg  
355 360 365

Lys Arg Leu Thr His Ser Glu Ala Tyr Pro His Phe Met Ser Ile Leu  
370 375 380

His His Cys Leu Gln Met Pro Tyr Lys Arg Ser Gly Asn Thr Val Gln  
385 390 395 400

Tyr Trp Leu Leu Leu Asp Arg Ile Ile Gln Gln Ile Val Ile Gln Asn  
405 410 415

Asp Lys Gly Gln Asp Pro Asp Ser Thr Pro Leu Glu Asn Phe Asn Ile  
420 425 430

Lys Asn Val Val Arg Met Leu Val Asn Glu Asn Glu Val Lys Gln Trp  
435 440 445

Lys Glu Gln Ala Glu Lys Met Arg Lys Glu His Asn Glu Leu Gln Gln  
450 455 460

Lys Leu Glu Lys Lys Glu Arg Glu Cys Asp Ala Lys Thr Gln Glu Lys  
465 470 475 480

Glu Glu Met Met Gln Thr Leu Asn Lys Met Lys Glu Lys Leu Glu Lys  
485 490 495



Glu Thr Thr Glu His Lys Gln Val Lys Gln Gln Val Ala Asp Leu Thr  
500 505 510

Ala Gln Leu His Glu Leu Ser Arg Arg Ala Val Cys Ala Ser Ile Pro  
515 520 525

Gly Gly Pro Ser Pro Gly Ala Pro Gly Gly Pro Phe Pro Ser Ser Val  
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Pro Gly Ser Leu Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro Gly Gly  
545 550 555 560

Met Leu Pro Pro Pro Pro Pro Pro Leu Pro Pro Gly Gly Pro Pro Pro  
565 570 575

Pro Pro Gly Pro Pro Pro Leu Gly Ala Ile Met Pro Pro Pro Gly Ala  
580 585 590

Pro Met Gly Leu Ala Leu Lys Lys Lys Ser Ile Pro Gln Pro Thr Asn  
595 600 605

Ala Leu Lys Ser Phe Asn Trp Ser Lys Leu Pro Glu Asn Lys Leu Glu  
610 615 620

Gly Thr Val Trp Thr Glu Ile Asp Asp Thr Lys Val Phe Lys Ile Leu  
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Asp Phe Phe Val Asn Ser Asn Ser Lys Gln Lys Glu Ala Asp Ala Ile  
660 665 670

Asp Asp Thr Leu Ser Ser Lys Leu Lys Val Lys Glu Leu Ser Val Ile  
675 680 685

Asp Gly Arg Arg Ala Gln Asn Cys Asn Ile Leu Leu Ser Arg Leu Lys  
690 695 700

Leu Ser Asn Asp Glu Ile Lys Arg Ala Ile Leu Thr Met Asp Glu Gln  
705 710 715 720

Glu Asp Leu Pro Lys Asp Met Leu Glu Gln Leu Leu Lys Phe Val Pro  
725 730 735

Glu Lys Ser Asp Ile Asp Leu Leu Glu Glu His Lys His Glu Leu Asp  
740 745 750

Arg Met Ala Lys Ala Asp Arg Phe Leu Phe Glu Met Ser Arg Ile Asn

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Glu Arg Val Ala Glu Val Lys Pro Lys Val Glu Ala Ile Arg Ser Gly 785 790 795 800		
Ser Glu Glu Val Phe Arg Ser Gly Ala Leu Lys Gln Leu Leu Glu Val 805 810 815		
Val Leu Ala Phe Gly Asn Tyr Met Asn Lys Gly Gln Arg Gly Asn Ala 820 825 830		
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Ser Ile Asp Lys Asn Ile Thr Leu Leu His Tyr Leu Ile Thr Ile Val 850 855 860		
Glu Asn Lys Tyr Pro Ser Val Leu Asn Leu Asn Glu Glu Leu Arg Asp 865 870 875 880		
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Gln Lys Ser Gln Pro Pro Gln Pro Gly Asp Lys Phe Val Ser Val Val 915 920 925		
Ser Gln Phe Ile Thr Val Ala Ser Phe Ser Phe Ser Asp Val Glu Asp 930 935 940		
Leu Leu Ala Glu Ala Lys Asp Leu Phe Thr Lys Ala Val Lys His Phe 945 950 955 960		
Gly Glu Glu Ala Gly Lys Ile Gln Pro Asp Glu Phe Phe Gly Ile Phe 965 970 975		
Asp Gln Phe Leu Gln Ala Val Ser Glu Ala Lys Gln Glu Asn Glu Asn 980 985 990		
Met Arg Lys Lys Lys Glu Glu Glu Glu Arg Arg Ala Arg Met Glu Ala 995 1000 1005		
Gln Leu Lys Glu Gln Arg Glu Arg Glu Arg Lys Met Arg Lys Ala 1010 1015 1020		
Lys Glu Asn Ser Glu Glu Ser Gly Glu Phe Asp Asp Leu Val Ser		

1025                      1030                      1035

Ala Leu Arg Ser Gly Glu Val Phe Asp Lys Asp Leu Ser Lys Leu  
 1040                      1045                      1050

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<213> NM\_002122 MHC class II DQ alpha 1, HLA-DQA1

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<400> 67

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 1                      5                      10                      15

gtg atg agc ccc tgt gga ggt gaa gac att gtg gct gac cac gtt gcc 96  
 Val Met Ser Pro Cys Gly Gly Glu Asp Ile Val Ala Asp His Val Ala  
                     20                      25                      30

tct tgt ggt gta aac ttg tac cag ttt tac ggt ccc tct ggc cag tac 144  
 Ser Cys Gly Val Asn Leu Tyr Gln Phe Tyr Gly Pro Ser Gly Gln Tyr  
                     35                      40                      45

acc cat gaa ttt gat gga gat gag cag ttc tac gtg gac ctg gag agg 192  
 Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu Glu Arg  
                     50                      55                      60

aag gag act gcc tgg cgg tgg cct gag ttc agc aaa ttt gga ggt ttt 240  
 Lys Glu Thr Ala Trp Arg Trp Pro Glu Phe Ser Lys Phe Gly Gly Phe  
 65                      70                      75                      80

gac ccg cag ggt gca ctg aga aac atg gct gtg gca aaa cac aac ttg 288  
 Asp Pro Gln Gly Ala Leu Arg Asn Met Ala Val Ala Lys His Asn Leu  
                     85                      90                      95

aac atc atg att aaa cgc tac aac tct acc gct gct acc aat gag gtt 336  
 Asn Ile Met Ile Lys Arg Tyr Asn Ser Thr Ala Ala Thr Asn Glu Val  
                     100                      105                      110

cct gag gtc aca gtg ttt tcc aag tct ccc gtg aca ctg ggt cag ccc 384  
 Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro  
                     115                      120                      125

aac acc ctc att tgt ctt gtg gac aac atc ttt cct cct gtg gtc aac 432  
 Asn Thr Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val Asn  
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 Ile Thr Trp Leu Ser Asn Gly Gln Ser Val Thr Glu Gly Val Ser Glu  
 145 150 155 160  
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 Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Tyr  
 165 170 175  
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 Leu Thr Phe Leu Pro Ser Ala Asp Glu Ile Tyr Asp Cys Lys Val Glu  
 180 185 190  
 cac tgg ggc ctg gac cag cct ctt ctg aaa cac tgg gag cct gag att 624  
 His Trp Gly Leu Asp Gln Pro Leu Leu Lys His Trp Glu Pro Glu Ile  
 195 200 205  
 cca gcc cct atg tca gag ctc aca gag act gtg gtc tgt gcc ctg ggg 672  
 Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu Gly  
 210 215 220  
 ttg tct gtg ggc ctc atg ggc att gtg gtg ggc act gtc ttc atc atc 720  
 Leu Ser Val Gly Leu Met Gly Ile Val Val Gly Thr Val Phe Ile Ile  
 225 230 235 240  
 caa ggc ctg cgt tca gtt ggt gct tcc aga cac caa ggg cca ttg 765  
 Gln Gly Leu Arg Ser Val Gly Ala Ser Arg His Gln Gly Pro Leu  
 245 250 255  
 tgaatcccat cctggaaggg aagggtgcac gccatctaca ggagcagaag aatggacttg 825  
 ctaaatagacc tagcactatt ctctggcccc atttatcata tcccttttct cctccaaata 885  
 tttctcctct caccttttct ctgggactta agctgctata tcccctcaga gctcacaaat 945  
 gcctttacat tctttccctg acctcctgat tttttttttc tttttctcaa tgttacctac 1005  
 aatacatgcc tggggtaagc caccgggcta cctaattcct cagtaacctc catctaaaat 1065  
 ctccaaggaa gcaataaatt ccttttatga g 1096

&lt;210&gt; 68

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; NM\_002122 MHC class II DQ alpha 1, HLA-DQA1

&lt;400&gt; 68

Met Ile Leu Asn Lys Ala Leu Leu Leu Gly Ala Leu Ala Leu Thr Thr  
 1 5 10 15

Val Met Ser Pro Cys Gly Gly Glu Asp Ile Val Ala Asp His Val Ala  
 20 25 30

Ser Cys Gly Val Asn Leu Tyr Gln Phe Tyr Gly Pro Ser Gly Gln Tyr  
 35 40 45

Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu Glu Arg  
 50 55 60

Lys Glu Thr Ala Trp Arg Trp Pro Glu Phe Ser Lys Phe Gly Gly Phe  
 65 70 75 80

Asp Pro Gln Gly Ala Leu Arg Asn Met Ala Val Ala Lys His Asn Leu  
 85 90 95

Asn Ile Met Ile Lys Arg Tyr Asn Ser Thr Ala Ala Thr Asn Glu Val  
 100 105 110

Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro  
 115 120 125

Asn Thr Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val Asn  
 130 135 140

Ile Thr Trp Leu Ser Asn Gly Gln Ser Val Thr Glu Gly Val Ser Glu  
 145 150 155 160

Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Tyr  
 165 170 175

Leu Thr Phe Leu Pro Ser Ala Asp Glu Ile Tyr Asp Cys Lys Val Glu  
 180 185 190

His Trp Gly Leu Asp Gln Pro Leu Leu Lys His Trp Glu Pro Glu Ile  
 195 200 205

Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu Gly  
 210 215 220

Leu Ser Val Gly Leu Met Gly Ile Val Val Gly Thr Val Phe Ile Ile  
 225 230 235 240

Gln Gly Leu Arg Ser Val Gly Ala Ser Arg His Gln Gly Pro Leu  
 245 250 255

<210> 69

<211> 2820

<212> DNA

<213> NM\_003014 SFRP4, secreted frizzled-related protein 4

<220>

<221> CDS

&lt;222&gt; (238) .. (1275)

&lt;223&gt;

&lt;400&gt; 69

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cggagctccg cggccggacc ccgcggcccc gctttgtctc cgactggagt ttgggggaag      120
aaactctcct gcgccccaga agatttcttc ctcggcgaag ggacagcgaa agatgagggt      180
ggcaggaaga gaaggcgctt tctgtctgcc ggggtcgcag cgcgagaggg cagtgcc          237
atg ttc ctc tcc atc cta gtg gcg ctg tgc ctg tgg ctg cac ctg gcg          285
Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
1      5      10      15
ctg ggc gtg cgc ggc gcg ccc tgc gag gcg gtg cgc atc cct atg tgc          333
Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
20      25      30
cgg cac atg ccc tgg aac atc acg cgg atg ccc aac cac ctg cac cac          381
Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
35      40      45
agc acg cag gag aac gcc atc ctg gcc atc gag cag tac gag gag ctg          429
Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
50      55      60
gtg gac gtg aac tgc agc gcc gtg ctg cgc ttc ttc ttc tgt gcc atg          477
Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
65      70      75      80
tac gcg ccc att tgc acc ctg gag ttc ctg cac gac cct atc aag ccg          525
Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
85      90      95
tgc aag tcg gtg tgc caa cgc gcg cgc gac gac tgc gag ccc ctc atg          573
Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
100      105      110
aag atg tac aac cac agc tgg ccc gaa agc ctg gcc tgc gac gag ctg          621
Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
115      120      125
cct gtc tat gac cgt ggc gtg tgc att tcg cct gaa gcc atc gtc acg          669
Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
130      135      140
gac ctc ccg gag gat gtt aag tgg ata gac atc aca cca gac atg atg          717
Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
145      150      155      160
gta cag gaa agg cct ctt gat gtt gac tgt aaa cgc cta agc ccc gat          765
Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
165      170      175
cgg tgc aag tgt aaa aag gtg aag cca act ttg gca acg tat ctc agc          813
Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
180      185      190
aaa aac tac agc tat gtt att cat gcc aaa ata aaa gct gtg cag agg          861
Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
195      200      205
agt ggc tgc aat gag gtc aca acg gtg gtg gat gta aaa gag atc ttc          909

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gacagttggg atactttaat cagaaaaaaa gaacttattt gcagcatttt atcaacaaat 2375  
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 taacacagta agcatgtatt ttataaggca ttcaataaat gcacaacgcc caaaggaaat 2495  
 aaaatcctat ctaatcctac tctccactac acagaggtaa tcactattag tattttggca 2555  
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 aacctgtata catgtgtttc ataacctgcc tcctttgctt ggccttttat tgagataagt 2675  
 tttcctgtca agaaagcaga aaccatctca tttctaacag ctgtgttata ttccatagta 2735  
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<210> 70

<211> 346

<212> PRT

<213> NM\_003014 SFRP4, secreted frizzled-related protein 4

<400> 70

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 20 25 30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His  
 35 40 45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu  
 50 55 60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met  
 65 70 75 80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro  
 85 90 95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met  
 100 105 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu  
 115 120 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr  
 130 135 140



Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met  
 145 150 155 160

Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp  
 165 170 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser  
 180 185 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg  
 195 200 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe  
 210 215 220

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn  
 225 230 235 240

Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile  
 245 250 255

Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu  
 260 265 270

Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu  
 275 280 285

Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr  
 290 295 300

Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro  
 305 310 315 320

Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser  
 325 330 335

Ala Gln Lys Arg Thr Asn Pro Lys Arg Val  
 340 345

<210> 71

<211> 1362

<212> DNA

<213> NM\_004039 annexin A2

<220>

<221> CDS

<222> (50)..(1066)

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Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser Thr  
5 10 15

ccc cca agt gca tat ggg tct gtc aaa gcc tat act aac ttt gat gct 154  
Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn Phe Asp Ala  
20 25 30 35

gag cgg gat gct ttg aac att gaa aca gcc atc aag acc aaa ggt gtg 202  
Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr Lys Gly Val  
40 45 50

gat gag gtc acc att gtc aac att ttg acc aac cgc agc aat gca cag 250  
Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser Asn Ala Gln  
55 60 65

aga cag gat att gcc ttc gcc tac cag aga agg acc aaa aag gaa ctt 298  
Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys Lys Glu, Leu  
70 75 80

gca tca gca ctg aag tca gcc tta tct ggo cac ctg gag acg gtg att 346  
Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu Thr Val Ile  
85 90 95

ttg ggc cta ttg aag aca cct gct cag tat gac gct tct gag cta aaa 394  
Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser Glu Leu Lys  
100 105 110 115

gct tcc atg aag ggg ctg gga acc gac gag gac tct ctc att gag atc 442  
Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu Ile Glu Ile  
120 125 130

atc tgc tcc aga acc aac cag gag ctg cag gaa att aac aga gtc tac 490  
Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn Arg Val Tyr  
135 140 145

aag gaa atg tac aag act gat ctg gag aag gac att att tcg gac aca 538  
Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile Ser Asp Thr  
150 155 160

tct ggt gac ttc cgc aag ctg atg gtt gcc ctg gca aag ggt aga aga 586  
Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys Gly Arg Arg  
165 170 175

gca gag gat ggc tct gtc att gat tat gaa ctg att gac caa gat gct 634  
Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp Gln Asp Ala  
180 185 190 195

cgg gat ctc tat gac gct gga gtg aag agg aaa gga act gat gtt ccc 682  
 Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr Asp Val Pro  
 200 205 210

aag tgg atc agc atc atg acc gag cgg agc gtg ccc cac ctc cag aaa . 730  
Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His Leu Gln Lys  
215 220 225

gta ttt gat agg tac aag agt tac agc cct tat gac atg ttg gaa agc 778  
Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met Leu Glu Ser  
230 235 240

atc agg aaa gag gtt aaa gga gac ctg gaa aat gct ttc ctg aac ctg 826  
 Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe Leu Asn Leu  
 245 250 255

gtt cag tgc att cag aac aag ccc ctg tat ttt gct gat cgg ctg tat 874  
 Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp Arg Leu Tyr  
 260 265 270 275

gac tcc atg aag ggc aag ggg acg cga gat aag gtc ctg atc aga atc 922  
 Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu Ile Arg Ile  
 280 285 290

atg gtc tcc cgc agt gaa gtg gac atg ttg aaa att agg tct gaa ttc 970  
 Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg Ser Glu Phe  
 295 300 305

aag aga aag tac ggc aag tcc ctg tac tat tat atc cag caa gac act 1018  
 Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln Gln Asp Thr  
 310 315 320

aag ggc gac tac cag aaa gcg ctg ctg tac ctg tgt ggt gga gat gac 1066  
 Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly Gly Asp Asp  
 325 330 335

tgaagcccgga cacggcctga gcgtccagaa atgggtgctca ccatgcttcc agctaacagg 1126

tctagaaaac cagcttgcca ataacagtcc ccgtggccat ccctgtgagg gtgacgttag 1186

cattaccccc aacctcattt tagttgccta agcattgcct ggccttctctg tctagtctct 1246

cctgtaagcc aaagaaatga acattccaag gagttggaag tgaagtctat gatgtgaaac 1306

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<210> 72

<211> 339

<212> PRT

<213> NM\_004039 annexin A2

<400> 72

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His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn  
 20 25 30

Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr  
 35 40 45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser  
 50 55 60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys  
 65 70 75 80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu  
85 90 95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser  
100 105 110

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu  
115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn  
130 135 140

Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile  
145 150 155 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys  
165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp  
180 185 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr  
195 200 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His  
210 215 220

Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met  
225 230 235 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe  
245 250 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp  
260 265 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu  
275 280 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg  
290 295 300

Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln  
305 310 315 320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly  
325 330 335

Gly Asp Asp

&lt;210&gt; 73

&lt;211&gt; 850

&lt;212&gt; DNA

&lt;213&gt; NM\_003955 SOCS3

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (107)..(781)

&lt;223&gt;

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 Met Val Thr  
 1  
 cac agc aag ttt ccc gcc gcc ggg atg agc cgc ccc ctg gac acc agc 163  
 His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu Asp Thr Ser  
 5 10 15  
 ctg cgc ctc aag acc ttc agc tcc aag agc gag tac cag ctg gtg gtg 211  
 Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln Leu Val Val  
 20 25 30 35  
 aac gca gtg cgc aag ctg cag gag agc ggc ttc tac tgg agc gca gtg 259  
 Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp Ser Ala Val  
 40 45 50  
 acc ggc ggc gag gcg aac ctg ctg ctc agt gcc gag ccc gcc ggc acc 307  
 Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro Ala Gly Thr  
 55 60 65  
 ttt ctg atc cgc gac agc tcg gac cag cgc cac ttc ttc acg ctc agc 355  
 Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe Thr Leu Ser  
 70 75 80  
 gtc aag acc cag tct ggg acc aag aac ctg cgc atc cag tgt gag ggg 403  
 Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln Cys Glu Gly  
 85 90 95  
 ggc agc ttc tct ctg cag agc gat ccc cgg agc acg cag ccc gtg ccc 451  
 Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln Pro Val Pro  
 100 105 110 115  
 cgc ttc gac tgc gtg ctc aag ctg gtg tac cac tac atg ccg ccc cct 499  
 Arg Phe Asp Cys Val Leu Lys Leu Val Tyr His Tyr Met Pro Pro Pro  
 120 125 130  
 gga gcc ccc tcc ttc ccc tcg cca cct act gaa ccc tcc tcc gag gtg 547  
 Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser Ser Glu Val  
 135 140 145  
 ccc gag cag ccg tct gcc cag cca ctc cct ggg agt ccc ccc aga aga 595  
 Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro Pro Arg Arg  
 150 155 160  
 gcc tat tac atc tac tcc ggg ggc gag aag atc ccc ctg gtg ttg agc 643

Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu Val Leu Ser  
 165 170 175

cgg ccc ctc tcc tcc aac gtg gcc act ctt cag cat ctc tgt cgg aag 691  
 Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu Cys Arg Lys  
 180 185 190 195

acc gtc aac ggc cac ctg gac tcc tat gag aaa gtc acc cag ctg ccg 739  
 Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr Gln Leu Pro  
 200 205 210

ggg ccc att cgg gag ttc ctg gac cag tac gat gcc ccg ctt 781  
 Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro Leu  
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<210> 74

<211> 225

<212> PRT

<213> NM\_003955 SOCS3

<400> 74

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 20 25 30

Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp  
 35 40 45

Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro  
 50 55 60

Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe  
 65 70 75 80

Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln  
 85 90 95

Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln  
 100 105 110

Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val Tyr His Tyr Met  
 115 120 125

Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser  
 130 135 140

Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro  
 145 150 155 160

Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu  
 165 170 175

Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu  
 180 185 190

Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr  
 195 200 205

Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro  
 210 215 220

Leu  
 225

<210> 75

<211> 369

<212> DNA

<213> NM\_000331. SAA1, serum amyloid A1

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 75

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 1 5 10 15

agc agc cga agc ttc ttt tgc ttc ctt ggc gag gct ttt gat ggg gct 96  
 Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala  
 20 25 30

cgg gac atg tgg aga gcc tac tct gac atg aga gaa gcc aat tac atc 144  
 Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile  
 35 40 45

ggc tca gac aaa tac ttc cat gct cgg ggg aac tat gat gct gcc aaa 192  
 Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys  
 50 55 60

agg gga cct ggg ggt gtc tgg gct gca gaa gcg atc agc gat gcc aga 240  
 Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg  
 65 70 75 80

gag aat atc cag aga ttc ttt ggc cat ggt gcg gag gac tcg ctg gct 288  
 Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala  
 85 90 95

gat cag gct gcc aat gaa tgg ggc agg agt ggc aaa gac ccc aat cac 336  
 Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His  
           100                                  105                                  110

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 Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr  
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<210> 76

<211> 122

<212> PRT

<213> NM\_000331 SAA1, serum amyloid A1

<400> 76

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           20                                  25                                  30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile  
           35                                  40                                  45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys  
           50                                  55                                  60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg  
           65                                  70                                  75                                  80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala  
           85                                  90                                  95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His  
           100                                  105                                  110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr  
           115                                  120

<210> 77

<211> 895

<212> DNA

<213> NM\_014059 RGC32

<220>

<221> CDS



&lt;222&gt; (147)..(497)

&lt;223&gt;

&lt;400&gt; 77

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cgcgccgggc ccagctgagc cgcctc atg aag ccg ccc gcg gag gac ctg tcg 173  
Met Lys Pro Pro Ala Glu Asp Leu Ser  
1 5

gac gcg ctg tgc gag ttt gac gcg gtg ctg gcc gac ttc gcg tcg ccc 221  
Asp Ala Leu Cys Glu Phe Asp Ala Val Leu Ala Asp Phe Ala Ser Pro  
10 15 20 25

ttc cac gag cgc cac ttc cac tac gag gag cac ctg gag cgc atg aag 269  
Phe His Glu Arg His Phe His Tyr Glu Glu His Leu Glu Arg Met Lys  
30 35 40

cgg cgc agc agc gcc agt gtc agc gac agc agc ggc ttc agc gac tcg 317  
Arg Arg Ser Ser Ala Ser Val Ser Asp Ser Ser Gly Phe Ser Asp Ser  
45 50 55

gag agt gca gat tca ctt tat agg aac agc ttc agc ttc agt gat gaa 365  
Glu Ser Ala Asp Ser Leu Tyr Arg Asn Ser Phe Ser Phe Ser Asp Glu  
60 65 70

aaa ctg aat tct cca aca gac tct acc cca gct ctt ctc tct gcc act 413  
Lys Leu Asn Ser Pro Thr Asp Ser Thr Pro Ala Leu Leu Ser Ala Thr  
75 80 85

gtc act cct cag aaa gct aaa tta gga gac aca aaa gag cta gaa gcc 461  
Val Thr Pro Gln Lys Ala Lys Leu Gly Asp Thr Lys Glu Leu Glu Ala  
90 95 100 105

ttc att gct gat ctt gac aaa act tta gca agt atg tgaacaaga 507  
Phe Ile Ala Asp Leu Asp Lys Thr Leu Ala Ser Met  
110 115

agttctgggt cctttcatca taaggagaa gcttcagaaa gttccgagga cctgctaaaa 567

tcagctacta gaatctgctg ccagagggga caaagacgtg cactcaacct tctaccaggc 627

cactctcagg ctcaccttaa aatcagccct tgatcccatt tctgggcaat ttagacagtg 687

aaactgactt tgtttacctg cttgcagcat attagaacag acgatccatg ctaatatgtt 747

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ttaattatat atagttggaa atagcagtaa gctttcccat tataatatat tttgtatac 867

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&lt;210&gt; 78

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; NM\_014059 RGC32

&lt;400&gt; 78

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 1 5 10 15

Ala Val Leu Ala Asp Phe Ala Ser Pro Phe His Glu Arg His Phe His  
 20 25 30

Tyr Glu Glu His Leu Glu Arg Met Lys Arg Arg Ser Ser Ala Ser Val  
 35 40 45

Ser Asp Ser Ser Gly Phe Ser Asp Ser Glu Ser Ala Asp Ser Leu Tyr  
 50 55 60

Arg Asn Ser Phe Ser Phe Ser Asp Glu Lys Leu Asn Ser Pro Thr Asp  
 65 70 75 80

Ser Thr Pro Ala Leu Leu Ser Ala Thr Val Thr Pro Gln Lys Ala Lys  
 85 90 95

Leu Gly Asp Thr Lys Glu Leu Glu Ala Phe Ile Ala Asp Leu Asp Lys  
 100 105 110

Thr Leu Ala Ser Met  
 115

&lt;210&gt; 79

&lt;211&gt; 1564

&lt;212&gt; DNA

&lt;213&gt; NM\_018004 FLJ10134

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (314)..(1138)

&lt;223&gt;

<400> 79  
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 acccaagtgtt aaaaattcct cccccactc aatgcgagac gtggccagat cccatccaac 180  
 acacggttta attttcatgg ggctctggga tcaaaagaac agaaacagca acaacaaaag 240  
 cccagccgct gtctgatttt aagctggcaa agtgggaaaa ataaagtgtt gagtaaacag 300  
 accaagttagg atc atg ggg aat ttc aga ggt cat gcc ctc cct gga acc 349  
 Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr  
 1 5 10

ttc ttt ttt att att ggt ctt tgg tgg tgt aca aag agt att ctg aag Phe Phe Phe Ile Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys 15 20 25	397
tat atc tgc aaa aag caa aag cga acc tgc tat ctt ggt tcc aaa aca Tyr Ile Cys Lys Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr 30 35 40	445
tta ttc tat cga ttg gaa att ttg gag gga att aca ata gtt ggc atg Leu Phe Tyr Arg Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met 45 50 55 60	493
gct tta act ggc atg gct ggg gag cag ttt att cct gga ggg ccc cat Ala Leu Thr Gly Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His 65 70 75	541
ctg atg tta tat gac tat aaa caa ggt cac tgg aat caa ctc ctg ggc Leu Met Leu Tyr Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly 80 85 90	589
tgg cat cat ttc acc atg tat ttc ttc ttt ggg ctg ttg ggt gtg gca Trp His His Phe Thr Met Tyr Phe Phe Gly Leu Leu Gly Val Ala 95 100 105	637
gat atc tta tgt ttc acc atc agt tca ctt cct gtg tcc tta acc aag Asp Ile Leu Cys Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys 110 115 120	685
tta atg ttg tca aat gcc tta ttt gtg gag gcc ttt atc ttc tac aac Leu Met Leu Ser Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn 125 130 135 140	733
cac act cat ggc cgg gaa atg ctg gac atc ttt gtg cac cag ctg ctg His Thr His Gly Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu 145 150 155	781
gtt ttg gtc gtc ttt ctg aca ggc ctc gtt gcc ttc cta gag ttc ctt Val Leu Val Val Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu 160 165 170	829
gtt cgg aac aat gta ctt ctg gag cta ttg cgg tca agt ctc att ctg Val Arg Asn Asn Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu 175 180 185	877
ctt cag ggg agc tgg ttc ttt cag att gga ttt gtc ctg tat ccc ccc Leu Gln Gly Ser Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro 190 195 200	925
agt gga ggt cct gca tgg gat ctg atg gat cat gaa aat att ttg ttt Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe 205 210 215 220	973
ctc acc ata tgc ttt tgt tgg cat tat gca gta acc att gtc atc gtt Leu Thr Ile Cys Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val 225 230 235	1021
gga atg aat tat gct ttc att acc tgg ttg gtt aaa tct aga ctt aag Gly Met Asn Tyr Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys 240 245 250	1069
agg ctc tgc tcc tca gaa gtt gga ctt ctg aaa aat gct gaa cga gaa Arg Leu Cys Ser Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu 255 260 265	1117
caa gaa tca gaa gaa gaa atg tgactttgat gagcttccag tttttctaga Gln Glu Ser Glu Glu Glu Met 270 275	1168

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<210> 80

<211> 275

<212> PRT

<213> NM\_018004 FLJ10134

<400> 80

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 20 25 30  
 Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg  
 35 40 45  
 Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly  
 50 55 60  
 Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr  
 65 70 75 80  
 Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe  
 85 90 95  
 Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys  
 100 105 110  
 Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser  
 115 120 125  
 Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly  
 130 135 140  
 Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val  
 145 150 155 160

Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn  
 165 170 175

Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser  
 180 185 190

Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro  
 195 200 205

Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys  
 210 215 220

Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr  
 225 230 235 240

Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser  
 245 250 255

Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu  
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Glu Glu Met  
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<210> 81

<211> 2311

<212> DNA

<213> NM\_004004 GJB2, connexin 26

<220>

<221> CDS

<222> (199)..(876)

<223>

<400> 81

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gtctccctgt tctgtcctag ctatgttcct gtgttggtgtg cattcgtctt ttccagagca 180

aaccgcccag agtagaag atg gat tgg ggc acg ctg cag acg atc ctg ggg 231  
 Met Asp Trp Gly Thr Leu Gln Thr Ile Leu Gly  
 1 5 10

ggt gtg aac aaa cac tcc acc agc att gga aag atc tgg ctc acc gtc 279  
 Gly Val Asn Lys His Ser Thr Ser Ile Gly Lys Ile Trp Leu Thr Val  
 15 20 25

ctc ttc att ttt cgc att atg atc ctc gtt gtg gct gca aag gag gtg 327

Leu Phe Ile Phe Arg Ile Met Ile Leu Val Val Ala Ala Lys Glu Val	
30 35 40	
tgg gga gat gag cag gcc gac ttt gtc tgc aac acc ctg cag cca ggc	375
Trp Gly Asp Glu Gln Ala Asp Phe Val Cys Asn Thr Leu Gln Pro Gly	
45 50 55	
tgc aag aac gtg tgc tac gat cac tac ttc ccc atc tcc cac atc cgg	423
Cys Lys Asn Val Cys Tyr Asp His Tyr Phe Pro Ile Ser His Ile Arg	
60 65 70 75	
cta tgg gcc ctg cag ctg atc ttc gtg tcc agc cca gcg ctc cta gtg	471
Leu Trp Ala Leu Gln Leu Ile Phe Val Ser Ser Pro Ala Leu Leu Val	
80 85 90	
gcc atg cac gtg gcc tac cgg aga cat gag aag aag agg aag ttc atc	519
Ala Met His Val Ala Tyr Arg Arg His Glu Lys Lys Arg Lys Phe Ile	
95 100 105	
aag ggg gag ata aag agt gaa ttt aag gac atc gag gag atc aaa acc	567
Lys Gly Glu Ile Lys Ser Glu Phe Lys Asp Ile Glu Glu Ile Lys Thr	
110 115 120	
cag aag gtc cgc atc gaa gcc tcc ctg tgg tgg acc tac aca agc agc	615
Gln Lys Val Arg Ile Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser	
125 130 135	
atc ttc ttc cgg gtc atc ttc gaa gcc gcc ttc atg tac gtc ttc tat	663
Ile Phe Phe Arg Val Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr	
140 145 150 155	
gtc atg tac gac gcc ttc tcc atg cag cgg ctg gtg aag tgc aac gcc	711
Val Met Tyr Asp Gly Phe Ser Met Gln Arg Leu Val Lys Cys Asn Ala	
160 165 170	
tgg cct tgt ccc aac act gtg gac tgc ttt gtg tcc cgg ccc acg gag	759
Trp Pro Cys Pro Asn Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu	
175 180 185	
aag act gtc ttc aca gtg ttc atg att gca gtg tct gga att tgc atc	807
Lys Thr Val Phe Thr Val Phe Met Ile Ala Val Ser Gly Ile Cys Ile	
190 195 200	
ctg ctg aat gtc act gaa ttg tgt tat ttg cta att aga tat tgt tct	855
Leu Leu Asn Val Thr Glu Leu Cys Tyr Leu Leu Ile Arg Tyr Cys Ser	
205 210 215	
ggg aag tca aaa aag cca gtt taacgcattg ccagttgtt agattaagaa	906
Gly Lys Ser Lys Lys Pro Val	
220 225	
atagacagca tgagagggat gaggcaaccc gtgctcagct gtcaaggctc agtcgccagc	966
atttcccaac acaaagattc tgaccttaaa tgcaaccatt tgaaaccctt gtaggcctca	1026
ggtgaaactc cagatgccac aatgagctct gctcccctaa agcctcaaaa caaaggccta	1086
attctatgcc tgtcttaatt ttctttcact taagttagtt ccaactgagac ccaggtgt	1146
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ttacactttt tggaagtga aactttgtag tatgataggt tattttgatg taaagatggt	1446

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 agggttaagta ttttctgtt gtcaagaata gcattgtaaa agcattttgt aataataaag 2226  
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<210> 82

<211> 226

<212> PRT

<213> NM\_004004 GJB2, connexin 26

<400> 82

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 20 25 30

Ile Met Ile Leu Val Val Ala Ala Lys Glu Val Trp Gly Asp Glu Gln  
 35 40 45

Ala Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys  
 50 55 60

Tyr Asp His Tyr Phe Pro Ile Ser His Ile Arg Leu Trp Ala Leu Gln  
 65 70 75 80

Leu Ile Phe Val Ser Ser Pro Ala Leu Leu Val Ala Met His Val Ala  
 85 90 95

Tyr Arg Arg His Glu Lys Lys Arg Lys Phe Ile Lys Gly Glu Ile Lys  
 100 105 110

Ser Glu Phe Lys Asp Ile Glu Glu Ile Lys Thr Gln Lys Val Arg Ile  
 115 120 125

Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Val  
 130 135 140

Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Val Met Tyr Asp Gly  
 145 150 155 160

Phe Ser Met Gln Arg Leu Val Lys Cys Asn Ala Trp Pro Cys Pro Asn  
 165 170 175

Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu Lys Thr Val Phe Thr  
 180 185 190

Val Phe Met Ile Ala Val Ser Gly Ile Cys Ile Leu Leu Asn Val Thr  
 195 200 205

Glu Leu Cys Tyr Leu Leu Ile Arg Tyr Cys Ser Gly Lys Ser Lys Lys  
 210 215 220

Pro Val  
 225

<210> 83

<211> 2389

<212> DNA

<213> NM\_002514 NOV1, neuroblastoma overexpressed gene

<220>

<221> CDS

<222> (73)..(1143)

<223>

<400> 83

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 Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys  
 1 5 10

cag tgc ctt tgc ctg acc ttc ctg ctt ctc cat ctc ctg gga cag gtc 159  
 Gln Cys Leu Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val  
 15 20 25

gct gcg act cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg 207



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acg	ccg	ccg	acc	tgc	gcc	ccc	ggg	gtg	cgc	gcg	gtg	ctg	gac	ggc	tgc	255
Thr	Pro	Pro	Thr	Cys 50	Ala	Pro	Gly	Val	Arg	Ala	Val	Leu	Asp	Gly	Cys	
tca	tgc	tgt	ctg	gtg	tgt	gcc	cgc	cag	cgt	ggc	gag	agc	tgc	tca	gat	303
Ser	Cys	Cys	Leu	Val	Cys	Ala	Arg	Gln	Arg	Gly	Glu	Ser	Cys	Ser	Asp	
ctg	gag	cca	tgc	gac	gag	agc	agt	ggc	ctc	tac	tgt	gat	cgc	agc	gcg	351
Leu	Glu	Pro	Cys	Asp	Glu	Ser	Ser	Gly	Leu	Tyr	Cys	Asp	Arg	Ser	Ala	
gac	ccc	agc	aac	cag	act	ggc	atc	tgc	acg	gcg	gta	gag	gga	gat	aac	399
Asp	Pro	Ser	Asn	Gln	Thr	Gly	Ile	Cys	Thr	Ala	Val	Glu	Gly	Asp	Asn	
tgt	gtg	ttc	gat	ggg	gtc	atc	tac	cgc	agt	gga	gag	aaa	ttt	cag	cca	447
Cys	Val	Phe	Asp	Gly	Val	Ile	Tyr	Arg	Ser	Gly	Glu	Lys	Phe	Gln	Pro	
agc	tgc	aaa	ttc	cag	tgc	acc	tgc	aga	gat	ggg	cag	att	ggc	tgt	gtg	495
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Pro	Arg	Cys	Gln	Leu	Asp	Val	Leu	Pro	Glu	Pro	Asn	Cys	Pro	Ala		
cca	aga	aaa	gtt	gag	gtg	cct	gga	gag	tgc	tgt	gaa	aag	tgg	atc	tgt	591
Pro	Arg	Lys	Val	Glu	Val	Pro	Gly	Glu	Cys	Cys	Glu	Lys	Trp	Ile	Cys	
ggc	cca	gat	gag	gag	gat	tca	ctg	gga	ggc	ctt	acc	ctt	gca	gct	tac	639
Gly	Pro	Asp	Glu	Glu	Asp	Ser	Leu	Gly	Gly	Leu	Thr	Leu	Ala	Ala	Tyr	
agg	cca	gaa	gcc	acc	cta	gga	gta	gaa	gtc	tct	gac	tca	agt	gtc	aac	687
Arg	Pro	Glu	Ala	Thr	Leu	Gly	Val	Glu	Val	Ser	Asp	Ser	Ser	Val	Asn	
tgc	att	gaa	cag	acc	aca	gag	tgg	aca	gca	tgc	tcc	aag	agc	tgt	ggc	735
Cys	Ile	Glu	Gln	Thr	Thr	Glu	Trp	Thr	Ala	Cys	Ser	Lys	Ser	Cys	Gly	
atg	ggg	ttc	tcc	acc	cgg	gtc	acc	aat	agg	aac	cgt	caa	tgt	gag	atg	783
Met	Gly	Phe	Ser	Thr	Arg	Val	Thr	Asn	Arg	Asn	Arg	Gln	Cys	Glu	Met	
ctg	aaa	cag	act	cgg	ctc	tgc	atg	gtg	cgg	ccc	tgt	gaa	caa	gag	cca	831
Leu	Lys	Gln	Thr	Arg	Leu	Cys	Met	Val	Arg	Pro	Cys	Glu	Gln	Glu	Pro	
gag	cag	cca	aca	gat	aag	aaa	gga	aaa	aag	tgt	ctc	cgc	acc	aag	aag	879
Glu	Gln	Pro	Thr	Asp	Lys	Lys	Gly	Lys	Lys	Cys	Leu	Arg	Thr	Lys	Lys	
tca	ctc	aaa	gcc	atc	cac	ctg	cag	ttc	aag	aac	tgc	acc	agc	ctg	cac	927
Ser	Leu	Lys	Ala	Ile	His	Leu	Gln	Phe	Lys	Asn	Cys	Thr	Ser	Leu	His	
acc	tac	aag	ccc	agg	ttc	tgt	ggg	gtc	tgc	agt	gat	ggc	cgc	tgc	tgc	975
Thr	Tyr	Lys	Pro	Arg	Phe	Cys	Gly	Val	Cys	Ser	Asp	Gly	Arg	Cys	Cys	
act	ccc	cac	aat	acc	aaa	acc	atc	cag	gca	gag	ttt	cag	tgc	tcc	cca	1023

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Gly	Gln	Ile	Val	Lys	Lys	Pro	Val	Met	Val	Ile	Gly	Thr	Cys	Thr	Cys	
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cac	acc	aac	tgt	cct	aag	aac	aat	gag	gcc	ttc	ctc	cag	gag	ctg	gag	1119
His	Thr	Asn	Cys	Pro	Lys	Asn	Asn	Glu	Ala	Phe	Leu	Gln	Glu	Leu	Glu	
	335					340					345					
ctg	aag	act	acc	aga	ggg	aaa	atg	taacctatca	ctcaagaagc	acacctacag						1173
Leu	Lys	Thr	Thr	Arg	Gly	Lys	Met									
350					355											
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aaaaaaaaaa	aaaaaa															2389

&lt;210&gt; 84

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; NM\_002514 NOV1, nephroblastoma overexpressed gene

&lt;400&gt; 84

Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys Gln Cys Leu  
1 5 10 15

Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val Ala Ala Thr  
20 25 30

Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro  
35 40 45

Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys  
50 55 60

Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro  
65 70 75 80

Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser  
85 90 95

Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn Cys Val Phe  
100 105 110

Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys  
115 120 125

Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys  
130 135 140

Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys  
145 150 155 160

Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp  
165 170 175

Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu  
180 185 190

Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn Cys Ile Glu  
195 200 205

Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe  
210 215 220

Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln  
225 230 235 240

Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro Glu Gln Pro  
245 250 255

Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys  
260 265 270

Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His Thr Tyr Lys  
275 280 285

Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His  
290 295 300

Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro Gly Gln Ile  
305 310 315 320

Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn  
325 330 335

Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu Leu Lys Thr  
340 345 350

Thr Arg Gly Lys Met  
355